STIC-Biotech/Ch mLib



94199

From: Sent: To: Subject: Hamud, Fozia Friday, May 16, 2003 9:48 AM STIC-Biotech/ChemLib sequence search for 09/912,157

RECEIVED HAY IS 2002

Please search 09/912,157, SEQ ID NO:2 amino acid residues 36-313, 36-753, 336-753 and 1-753 against commercial data bases and interference data bases. Thank you.

Fozia Hamud
Patent Examiner
Art Unit 1647
Crystal-Mall-One, Room 10Bo5
Mail Box CM1-10B19
308-8891

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: 5119
Date Completed: "51/9
Searcher Prep/Review!"/
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 4
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (where a	applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
www/Internet: 0	
Other (specify):	

· Y. ima. 1056

30 92.5 4.2 2314 1 A46151 brovican procein-tyrosine-p 52 4.2 888 2 85775 brovican precursor 32 4.2 888 2 A56777 brovican precursor 33 92 4.2 985 2 A56777 brovical procein statements of the procein sta	ALIGNMENTS	RESULT 1 T42695 hypothetical protein DKFZp434N1928.1 - human (fragment) C; Species: Homo sapiens (man) C; Accession: T42695 R; Bloecker, H; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database Rayember 1999, Mark A. Accession: T42695 A. Accession: T42695 A. Status: preliminary A. Molecule type: mRNA	A;Note: DKFZp434N1928.1 Query Match Best Local Similarity 100.0%; Score 2210; DB 2; Length 564; Best Local Similarity 100.0%; Pred. No. 3.6e-170; Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 KKKOGENIYSHIDEESSESSTYTAALPREKLRPRPKVFLCTSSKOOMBARVOCFAFFL 14.7 RKKOGENIYSHIDEESSESSTYTAALPREKLRPRPKVFLCTSSKOOMBARVOCFAFFL 61 ODFCGCEVALDLWEDFSLCREGOREWYJOKIHESOFIIVVCSKGKKYFVDKKNYKHKGGG 11111111111111111111111111111111	Db 267 RGSGKGELFLVAVSALAEKKROAKQSSAALSKFIAVTFDTSCEGDYFGILDLSTKTKLM 3.10. Qy 181 DNLPQLCSHLHSRDBGLQEPGQHTRQGSRRNTFRSKSGRSLTVAICNHQFIDEEPDWFE 240 Qy 181 DNLPQLCSHLHSRDBGLQEPGQHTRQGSRRNTFRSKSGRSLTVAICNHQFIDEEPDWFE 340 Qy 241 KQFVPFHPPPLRYREPVLEKEPDSGLYLNDVKCKPGPESDFCLKYGAAVLGATGPADSQHE 300 Qy 241 KQFVPFHPPPLRYREPVLEKEPDSGLYLNDVKCKPGPESDFCLKYGAAVLGATGPADSQHE 300 Qy 301 KQFVPFHPPPLRYREPVLHTIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	Gapop 10.0 , Gapext 0.5 Garched: 283224 seqs, 96134422 residues al number of hits satisfying chosen parameters: 283224	d by ch	s derived by analysis of the total score distribution. SUMMARIES Query Onery Descript	1 2210 100.0 564 2 742695 hypothetical prote 12.50.5 6.8 846 2 727282 hypothetical prote 13.126 5.7 718 2 730113 hypothetical prote 110 5.0 535 2 717212 hypothetical prote 110 5.0 535 2 717212 hypothetical prote 107.5 4.9 344.2 742730 hypothetical prote 105.5 4.8 592 2 742730 hospital protein vesicle transport 105 4.8 77 2 709081 telomere-associate 105 4.8 901 2 76093 dead ringer nuclea 2105 4.8 1571 2 744155 zinc finger protein	100.5 4.5 901 2 F83781 transposase 100.5 4.5 794 2 SS9069 transposase 29.5 4.4 291 2 F86451 protein Eds 20069 transposase 29.5 4.4 291 2 F86451 protein F881 2 F86599 protein F881 2 F86599 protein F881 2 F86599 protein F881 2 F881 2 F88145 protein F881 2 F88145 protein F881 2 F8814 protein F881 protein F881 2 F8814 protein F881 2 F8814 protein F881 protein F881 2 F8814 protein F8814 2

RESULT 2

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21.1%; Pred. No. 0.049;
tive 64; Mismatches 149; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       691 SESDSSESESESDNEG---EDPRITIVK 716
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A; Residues: 1-488; 489-535 <POU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: 218723
Best Local Similarity
Matches 82; Conserv
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A; Genetics:
A; Genetics:
C; Genetics: CESP: F64G10A.e
A; Introns: 106/1; 196/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3
C; Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                       C'Species: Caenorhabditis elegans
C'Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 20-Jun-2000
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Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DFCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGCGR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 -----RIMD-NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- LOAAISR 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 VLEKF------DSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             706 LKEKFAAKRDLEVEVLDSEDVKLLEDVKCAPGP----IHVEPTEPEVLEPAEEDMEEAE 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDV--PGILDLSTKY-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EPAIERITTGRND------VIFDMQCELALQHPCVISCHFSYIN 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 KINYIESDPOWFENTHHRVATRRVSELEAHNIVPL-PPSLEVRVEDEDAFGOMETLPIDE 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKQQENIYSHLDEESSESSTYTAALPRERLRPRPRVFLCYSSKDGUHMAVVQCFAYFLQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 GGLDQDGEARPALDGSAA----LQPLL-HTVKAGSPSDMPRDSGIYDSS-VPSSELS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 ED-EEDEDDVDSVEGGTARIEELQRLIVH------KDMAHDSGNILDSATVSGSDFS 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 119;
                                                                                                                                                                                                                                                                                                           A)Cross-references: EMBL:AL110498; PIDN:CAB54470.1; CESP:Y64610A.e A:Experimental source: clone Y64610A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: CESP:F56D1.2
Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3
Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein Y64G10A.e - Caenorhabditis elegans
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...Chitsace, S.; Wilson, R.
ubmitted to the EMBL Data Library, November 1995
.Description: The sequence of C. elegans cosmid F56D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 6.8%; Score 150.5; DB 2; 11 Similarity 22.5%; Pred. No. 0.00065; 94; Conservative 57; Mismatches 147;
                                                                                                                                                                                                                              A.Status: preliminary; translated from GB/EMBL/DDBJ
A:Wolecule type: DNA
A:Residues: 1-846 <WIL)
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                                                                                  C; Accession: T7782;
R; Ainscough, R;
Submitted to the EMBL Data Library, September 1999
A; Reference number: 270336
A; Accession: T27282
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Residues: 1-718 <CHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Homo sapiens (man)
C; Date: 15-Oct.1999 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                       138 EKLRQAKOSSSAALSKFIAVTFDYSCEGDVP---GILDLSTKYRLMONLPQLCSHLHSRD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 LDQDGEARPALDGSAALQPLLHTVKAGSPSDM--PRDSGIYDSSVPSSELSLPLMEGLST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 - DED------DVDLQP--HASHQNQPLILLEPPEQCG------PDSD-----SD 690
                                                                                                                            398 RDKVRSREVRNIALTEFVKVMIVYAD-DNDLHTDCVKKLVENLRNCASCDPVFDLEKLIT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGLØEPGQHTRQGSRRNYFRSKSGRSLY---VAICNMHQFIDEEPDWFERQFVP---- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 FHPPPLRYREPVLEKFDSGLVLADVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 LH---LKRQSPVIVPIQT------EED---RIAASIKYNLVPPQALVDSD--- 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LCSHLHSRDHGLQE--PGQHTRQGSRRNYPRSKSGRSLYVAICNMHQFIDEEPDWFERQF 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 VPFH-PPPL------RIREPVLEKFDSGLVILNDVM---CKPGPESDFCLKVEAA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 VLGATG-PADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMP-----RD 340
                                                              RERLRPRP-----KVFLCTSSKDGQNHMNVQCFAYFLQDFCGCEVALDLMEDFS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 ATGASGLPAVSKAPS----MDAQQETHKSQDCLGLLDPLASA--AGVPSTAPMSGKKHRP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 SG-IYDSSVPSSELSLPLAEGLSTDQTETSSLTESVSSSSGLGEREPPALPSKLLSSG 397
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein DKFZp434P211.1 - human (fragments)
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101200000000000000000000000000000000000	Query Match A:8%; Score 105.5; DB 2; Length 592; Best Local Similarity 18.8%; Pred, No. 1.7; Matches 89; Conservative 60; Mismatches 145; Indels 179; Ga Qy 6 ENIXSHLDEESSESTYTAALPRERIRPREVELESGORHMAVOCFAFFLODFC- 1	176 AMARQIVTYCATLDENPGYRKSRPLDNASKLADUVEKKLEDYKKIDERGILKGKTGS 233 127 ELFLYAVSAIAEKLRQAKGSSSAALSKFIAVYFDSCEG-DVPGI 170 1	Db 378 ADGQRVEDSHLVILEVILNRHEDNCDKIRAVLLYIFGINGTFEEN	R; Sanchez Alonso, P.; Guzman, P. Genetics 148, 1043-1054, 1998 Genetics 148, 1043-1054, 1998 Genetics 148, 1043-1054, 1998 A; Title: Organization of chromosome ends in Ustilago maydis: recg-like helicase motiff A; Reference number: £1655; MUID:98198830; PMID:9539423 A; Reference number: £1655; MUID:98198830; PMID:9539423 A; Residues norginary; translated from GB/EMBL/DDBJ A; Residues: 1-75 - CSAN A; Residues: 1-75 - CSAN A; Residues: 1-75 - CSAN A; Cross references: SEBL:AF030885; NID:92642221; PID:92642222 A; Experimental source: strain FB2 C; Genetics: A; Genetics: UTASrecO C; Keywords: DNA binding	Ouery Match Best Local Similarity 20.6%; Pred. No. 2.6; Matches 92; Conservative 42; Mismatches 147; Indels 166; Gaps 23; Matches 92; Conservative 42; Mismatches 147; Indels 166; Gaps 23; Qy 11 HIDERSESSENTALP
A A DEMAND A CONTROL A C	RESULT 5 RESULT 5 RESULT 5 RESULT 5 RESULT 6 RESULT 7 RESULT	A; Residues; 1.3942 CDIED A; Cross references: EMBL:117034; NID:93413809; PIDN:CAA76598.1; PID:93413810 A; Experimental source: strain 129 SVJ A; Experimental spring spring content of the presynaptic cytoskeleton C; Function: may be involved in cytomatrix organization at the site of neurotransmitte A; Description: may be involved in cytomatrix organization at the site of neurotransmitte A; Description: may be involved in cytoskeleton C; Function: C; Function: C; Function: A; Description: may be involved in cytoskeleton C; Function: C; Function: A; Description: may be involved in cytoskeleton C; Function: C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: may be involved in cytoskeleton C; Function: A; Description: A; Descri	OY 181 DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSRSGRSLTVAICNMHQFIDEE 235	3692 POASPAPAMOKKGOPGYPSSADYSOSSRAPSAYHHASESKKGSRQAHTGPSALQPKADTO 330 KAGSPSDMPDSGIYDSSYPSSELSLPLMEGLSTDGTETSSLTESYSSSGLGEEBPPAL 3752 AQPQMQGRQAAPGPQSQPPSSRQTPSGTASRQPQTQQQQQQQGLGQQAPQQA 390 PSG 3811 3809 PSQ 3811	149.13 transport protein - mouse C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Accession: 149.239 C. Accession: 149.239 R. Fallam, J.T.; McIntosh, S.; James, D.E. J. Biol. Chem. 270, 5857-5863, 1995 A.Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neuron A.Reference number: 149.239 A.Status: preliminary; translated from GB/EMBL/DDBJ A. Status: preliminary; translated from GB/EMBL/DDBJ C. Genetics: L.592 - RESS A. Cross-references: EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g642028

1.44.4					<u> </u>
Qy 361 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSTTDE 411.	RESULT 9 T14155 zince finger protein Peg3 - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C; Date: 20-Sep-1999 R; Murodva, Y.; Kaneko-Ishino, T.; Kagitani, F.; Kohda, T.; Li, L.L.; Tada, M.; Suzuki NATLice: Peg3 imprinted gene on proximal chromosome 7 encodes for a zinc finger prote A; Mccession: T14155 A; Mccession: T18155 A; Mccession: T18155 A; Mcasiduce; A; Mcsiduce; A; Mcsiduc	Genetics: Genetics: Genetics: Genetics: Application: 7 Reywords: zinc finger A.8%; Score 105; DB 2; Length 1571; Best Local Similarity 19.2%; Pred. No. 7; Ratches 73; Conservative 49; Mismatches 135; Indels 124; Ga 71 DIMEDFSICREGOREWVIORIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGK 71 DIMEDFSIC	OY 126 GELFLVAVSAIAERILROARGSSSAALSKFIAVYPDYSCEDDYPGILDLSTKTRLADNLPQ 185 Db 552SRACEEFVPSQSLRRRQFYREXLFDENNARDA	Db 674 QKSHGGLGFSKPRPVAESSTQSSSSIYTPRAHSGGNTTEGKEKDSIIHSLPAPR 728 QY 334 PSDAPRDSGIYDSSYPSELSLPLAEGLSTDQTETSSITESYSSSGIG 382	RESULT 10 RESULT 10 FR3781 transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus FR3781 C.5pecies: Bacillus halodurans C.5Accession: F83781 R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Acids Res: 28, 4317-431, 2000 A.7Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A.7Seference number: A83650; MUID:20512582; PMID:11058132 A.5Etatus: preliminary A.Molecule type: DNA A.Residues: 1-901 <sto> A.Residues: 1-901 <sto 1-901="" <arresides="" a.residu<="" a.residues="" a.residues:="" td=""></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto>
Db :268 EMGCAAYSSESGSRADKAAIIODHICGKGSPVIVATSA	QY 193 RDBGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNHGQFIDEEDWFERQFYPFHPPLR 252 1 1 1 1 1 1 1 1 1 1	tein - fruit fly elanogaster quence_revision hak, R.D.; Kalio 2-799, 1996 on of the dead r	A; Residues: 1901 <pre>A; Reperter: 1902 <pre>A; Reperter: 1903 <pre>A; Reperter: 1904 <pre>A; Reperter: 1905 <pre< td=""><td>ARLYTARGGLVDY TRECANTORNER TRECANTORNER</td><td>Db 488. OGHVPVLGGHHPPQOQDGQQQQHHQQQQQSQQQHHLQQQRRSQSPDLSKHEALSA 547 QY 222 YVATCHMHQFIDEEDDWFEKQFVPFHPPPL</td></pre<></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>	ARLYTARGGLVDY TRECANTORNER	Db 488. OGHVPVLGGHHPPQOQDGQQQQHHQQQQQSQQQHHLQQQRRSQSPDLSKHEALSA 547 QY 222 YVATCHMHQFIDEEDDWFEKQFVPFHPPPL

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; Kagitani, F.; Kohda, T.; Li, L.L.; Tada, M.; Suzuki
                                                                                                                                                                                                                proximal chromosome 7 encodes for a zinc finger prote :96154192; PMID:8563758
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:vision 20-Sep-1999 #text_change 20-Sep-1999
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Pred. No. 7;
49; Mismatches 135; Indels 124; Gaps
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:AP001510; GB:BA000004; NID:g10173440; Strain:C;125	11 Db 264 GTDS
	RESULT 12
tich; 12.5%; Score 100.5; DB 2; Length 901; al.Similarity 22:6%; Pred. No. 7.6;	r48997 epsin-like prote
Matches 66; Conservative 44; Mismatches 103; Indels 79; Gaps 15;	N; Alternate name C; Species: Arabi
QYS-1 TRKQQENIXSHLDEESSESSTYTAALPRERLRPRAVFLCYSSKDGQN 48	C;Date: 02-Jun-2 C;Accession: T48 R:D'Angelo, M::
**************************************	submitted to the
	A; Accession: T48 A; Status: prelim
R8 - TOXTHERON TOWNS WIND WIND WAS A STATE OF THE STATE O	A; Molecule type:
597 DLSKTYRNROVYKOINMPIRKGEMVGLIGPNGAGRETTISMISSLIOPTSGDVLIK	
	C;Genetics: A;Gene: ATSP:F25
: : : : :	A, Map position: A; Introns: 12/2;
OY 188 SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLTVALCNMHQFIDEEP 236	Query Match Best Local Sim Matches 76;
DOCETTO 11	OY 85 EWIOR
ا د	DD 96 ERVIEE
C.Spectes: Mus musculus (house mouse)	0y 145 OSSSAA
Cidate: 4/-Apr-1390 #Sequence_revision 13-Mar-139/ #text_change 48-May-1399 CiAccession: S59069	::: Db 151 EKAAAN
Wells, J.R.E.	QY 197 LQEPGQ
Affitle: An unusual arrangement of 13 zinc fingers in the vertebrate gene zl3. Asseference number: S59069; NUID:96003919; PMID:7578457	Db 199 YRDDDR
	Qy 257 VLEKFD
A; MOLECULE LYPE: MAKNA A; Regidues: 1-794 <5675 A; Programming: TE: HIMEGE, MITH. SANDERS 1. DITH. SANDERS 1. DITH. SECOND 2.	DD 236 SVDNYN
Ajtrobs-reigrences: ds:ul4536; NID:go08136; FIDN:AAA83493.1; FID:go08137 C;Superfamily: POE domain homology P:10-108 //wwwsta: Dog Armain homology POES	OY 310 GEA
Chigary Match 4 68. Cooks 00 K. DB 3. Tonoth 704.	Db 287 QNIGAA
Similarity 20.6%; Pred. No. 7.7; Concernative 41; Mismatched 146; Indels 27, Cana	OY 367 ETSSLT
61	Db 339 AADFVN
D 24 CDCTFVVD-GVDF	
OY 123 SGRGELFLVAVSAIAERLROARGSSSAALSKFIAVYFDYSCEGDVPGILDLST 175	asisbi 666 qa
DD 68 AGLGQ	RESULT 13 F86451
176	protein F6N18.2 C;Species: Arabi
Db 107 achtlaslaepssttgesadasaveggdrrakderaaatmlsrlægargssstgpgrelk 166	C;Date: 02-Mar-2 C;Accession: F86
223 VAICNMHQFIDEEPDMFERQFVPEHPPPLRYREPVLEKFDSGLVIANDVMCKPGPESDFCL :	R, Theologis, A.; Chin, C.W.; Chu
Db 167 EERGGQARSASGABQTEKADAPREPPPVELKPDPTSSMA- 206	•
283 KVEAAVLGATGPADSQHESQHGGIDQDGEARPALDGSAALQPLLHTVRAGSPSDMPRDSG	A; Authors: Hunte C.A.; Li, J.H.;
DD 207 AAKAEALSESSEQEMEVEPASKGEDGQEEEGAGPATVKEEGHH-LDNGEPPEENEESA 263 Qy 343 IYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGGLGEE 384	Aizzo, M.; Roone A;Authors: Salzb ker, M.; Wu, D.;
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hung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alon hung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ughes, B.; Bulzar, L. Gonway, A.B.; Conn, C.; Khan, S.R.; Khaykin, E.; Kim, ter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, J.H., S.K.; Liu, E.A.; Luros, J.S.; Maiti, R.; Marzia ney, T.; Rowley, D.; Sawon, H. Sun, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
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                                                                                                                                                                                                                 ; Vezzl; A.; Modesto, D.; Pigazzl, M.; Valle, G.; Mewes, H.W.; Rudd, be Protein Sequence Database, May 2000 8997
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idopsis thaliana (mouse-ear cress)
2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
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ses protein P251.3-1.50
idopsis thaliana (mouse-ear cress)
2000 *sequence_revision 02-Jun-2000 *text_change 02-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARPAIDGSAALQPILHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRDKYHNSMHRPSGGYGDKYDYEG------RYGDRDEGRSSYGKEREYG 198
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ces: EMBL:AL356014; GSPDB:GN00061; ATSP:F25L23.150
source: cultivar Columbia; BAC clone F25L23
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DVFSPNPL 411
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;Coulie, P.G.; Lehmann, F.; Lethe, B.; Herman, J.; Lurquin, C.; Andrawiss, M.; Boon, roc. Natl. Acad. Sci. U. S.A. 92, 7976-7980, 1995.
Title: A mutated intron sequence codes for an antiqenic peptide recognized by cytol Reference number: 138944, MUID:95372402; PMID:7644523
Accession: 138945
Status: preliminary; translated from GB/EMBL/DDBJ
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A:Accession: 138946
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A;Cross-references: EMBL:U20908; NID:gl046218; PIDN:AAC50238.1; PID:gl046219
                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Howe sapiens (man)
C;bate: 31-May-1996 *sequence_revision 01-Dec-2000 *text_change 01-Dec-2000
C;Accession: I38945; I38946
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                                                                                                                                                                                              263 SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGS--- 319
                                                                              332 GSPSDMPRDSGIYDSS-----VPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.4%; Score 96.5; DB 2; Length 438;
Best Local Similarity 20.8%; Pred. No. 6.1%
Matches 94; Conservative 39; Mismatches 135; Indels 183; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SEPG--ECPAKKRPRLDGSQRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 VALDVLSEGSIWSQESSAGTGRADRSLRGKPMEHVSSPCDSNSSSLPRGDVLGSSRPHRR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 RPCVQQSLSSSFTCEKDPECKVDHKKGLRKSENPRGPLVLPAGGGAQDESGSRIHHKNWT 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GCEVALDINEDFSICREGOREWVIORIHESOFIIVVCSKCMKYFVDKKNYKHKGGGRGSG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GCK-----TYLCRWEKRLWPAKVLARTA------TSTKNKRRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 ------GQHTRQGSR---RNT-
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                                                                                                                                                                                                                                                                                                                                                                     melanoma ubiquitous mutated protein - human (fragment)
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A;Molecule type: DNA
A;Residues: 'G',1-74 <RE2>
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Job time: 22.4315 secs
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Rature 408, 816-820, 2008.
N; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.W.; Li, T.; Li, T.; Li, S.; Liu, E.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Atthers Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Telence number; Asidiali, Number, J.C.; Davis, R.W.

Térence number; Asidiali; Number, J.B.; PMID:11130712
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                                                                                                                                                                A;Cross.references: GB:AE005172; NID:q6714285; PIDN:AAF25981.1; GSPDB:GN00141 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE005173; NID: 98778302; PIDN: AAF79311.1; GSPDB: GN00141
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C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
C;Accession: F96599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 QSSLGDSGPNENOMOPSHDNQQQPQVEGQAQSHNHHSPRENDSARNTPILPTPKFDGPPQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337-WPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEBEPPALPSKLLSS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                          229 HQFIDEEPDWFEKQFVPFHPPPLRTREPVL---EKFDSGLVLNDVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 Q-----MHNNSLPS-----PRENGRGILPTPSQYRP--QSPTAYRNLLSPRSPSPLLST 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 AAVLGATGPADSQHESQHGGLDQ---DGEAR-----PALDGSAALQPLLHTVKAGSPSD 336
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ils of chromosome 1 of the plant Arabidopsis.
MOID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                      Indels 43;
                                                                                                                                                                                                                                                                                                                                 4.4%; Score 97.5; DB 2; Length 291; 24.2%; Pred. No. 2.9; 3.9; Indels 43
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             A; Title: Sequence and analysis of
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 24.28 hes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                A; Molecule type: DNA
A; Residues: 1-291 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-589 <STO>
                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tatus: preliminary
                                                                                                                                                                                                                                               A; Gene: F6N18.2
A; Map position: 1
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Matches
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Human interleukin Human interleukin Human Interleukin

Human interleukin

Murine cytokine re Human novel secret

Murine IL-17R prot Murine interleukin Murine interleukin

Murine IL-17R poly Murine Interleukin Murine interleukin

Human IL-17 recep

IL-17RH

Human

PRO polypepi EST encoded

Interleukin

PRO5801.

New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor

WPI; 2002-217048/27. N-PSDB; ABA95031, ABA95032.

Human Interleukin Human Interleukin

Human Interleukin

AAU09956 AAU09955 AAU09954 AAU09951 AAU09952

Murine interleukin

Human IL-17R

Scoring table:

Run on:

Searched:

Database:

Mouse interleukin Murine IL-17R prof

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Cytokine receptor; Leytor18; cell proliferation; antipsorlatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB07626
ID ABB07626 standard; Protein; 753 AA
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:
                                                                                                                                                                                                               May 19, 2003, 09:07:58; Search time 56.6401 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908470 seqs, 133250620 residues
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                                                                                                                                   OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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us-09-912-157-2.rag

growth, and modulating immune system by binding to ligand

Claim 1; Page 2; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Ecytori8. The Ecytori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psortasis or tumour growth. The encoding nucleic acids are useful for providing Ecytori8 in vivo by gene therapy techniques. Ecytori8 oligonicleotide probes are useful for in vivo diagnosis, and the Ecytori8 probes and primers can be used to detect and localize Ecytori8 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosoms 1 in which Ecytori8 gene resides. The Ecytori8-polymiciactions in chromosoms 1 in which inhapse-based testing of pulmonary alveolar proteinosis, familial polymorphisms of cytokine receptors. The present sequence represents a human Ecytori8 manto acid sequence.

753 AA; Sequence

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Gaps 9 1 MAPWIQICSVFFTVNACINGSQLAVAAGGSGRARGADTCGWRMKAAARPELCVANEGVGP 60 1 MAPWIQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP Query Match 100.0%; Score 4013; DB 23; Length 753; Best Local Similarity 100.0%; Pred. No. 0; Manatches 753; Conservative 0; Mismatches 0; Indels 0; à g

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180 121 FLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESOPFLNMKFETDYFVKVVPF g ŏ 8

PSIKNESNYHPFFFRTRACDLILIQPDNIACKPFWKPRNI.NISQHGSDMQVSFDHAPHNFG 181 셤 å

FRFFYLHYKLKHEGPFKRKTCKOEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300 241 ö 윱

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420 420 LPREKLRPRRYFLCYSSKDGONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 361 361 ò 셤

480 540 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 481 a ð

WVIQKIHESQFIIVVCSKGNKTFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480

171

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181

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9 QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL 541 ö 셤

VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660 601 ö 8

LHTVRAGSPSDNPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGERE

661

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721 PPALPSKLLSSGSCKADLGCRSTTDELHAVAPL 753 ò 용

Ź ABB07627 standard; Protein; 753

ABB07627;

20-MAY-2002 (first entry)

Human cytokine receptor, Zcytor18 variant sequence.

Cytokine receptor; Zcytoriß; cell proliferation; antipsoriatic; human pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.

Homo saplens.

Location/Qualifiers Misc-difference 269

/label- 1269M /note- "wild-type Thr is replaced with Met" /note- "wild-type Val is replaced with Ala" /note- "wild-type Val is replaced with Ala" Wisc-difference

WO200208259-A2

31-JAN-2002.

23-JUL-2001; 2001WO-US23253

26-JUL-2000; 2000US-220747P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE,

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WPI; 2002-217048/27. N-PSDB; ABA95033, ABA95034.

New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psortasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand

Disclosure; Page 94-98; 119pp; English.

designated Zcytoria The Zcytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit encoding uncleic acids are useful for providing Zcytoria be used to inhibit encoding nucleic acids are useful for providing Zcytoria in vivo by gene therapy techniques. Zcytoria oligonucleotide probes are useful for invivo diagnosis, and the Zcytoria probes and primers can be used to detect and localize Zcytoria gene expression in tissue samples. The probes are also used to detect and localize Zcytoria genes aberrations in chromosome 3 in which Ecytoria gene resides. The Zcytoria polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial polynociphisms of cytokine receptors. The present sequence represents a human Zcytoria variant amino acid sequence. The invention relates to an isolated cytokine receptor polypeptide

753 AA; Sequence

Gaps ö DB 23; Length 753; Indels ñ 99.8%; Score 4003; Ilarity 99.7%; Pred. No. 0; Conservative 0; Mismatches Similarity 751; Query Match Best Local Si Matches 751;

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23-JUL-2001; 2001WO-US23253;

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ASRNSGLYNITERYDNCTTYLNPVGRHVIADAQNITISOYACHDQVAVTILWSPGALGIE 120
                                                                                                                                PSIKNESNYHPEPERTRACDILIQPDNIACKPEWKPRNIJSGAGSDMQVSEDHAPHFG 240
                                                                                                                                                                                                                                  PLKGFRVILLEELKSEGROCOOLILKDPROLNSSFKRTGNESOPFLNMKFETDYFVKVVPF 180
                                                                                                      241 FRFFYLHTKIKHEGPFKRKTCKQEGTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
                                                                                                                                                                                         301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360
                                                                                                                                                                                                                                                                   LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGGRE 420
                                                                                                                                                                                                                                                                              361 LPRERLAPREVELCYSSKDGONHANVVQCFAYFLQDFCGCEVALDIMEDFSLCREGGRE 420
                                                                                                                                                                                                                                                                                                             WVIQKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPWILOLCSVFFTVNACINGSOLAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60
                . 1 MAPWIQICSVPFTVNACINGSQIAVAAGGSGRARGADTCGWRMKAAARPRICVANEGVGP 60
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Cytokine receptor; Ecytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinos1s; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
                                                                                                Human cytokine receptor, Zcytor18 splice variant.
                     ABB07628 standard; Protein; 739 AA
                                                                        (first entry)
                                                                                                                                                                          Homo sapiens.
                                                                        20-MAY-2002
                                               ABB07628;
RESULT 3
ABB07628
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WO200208259-A2

31-JAN-2002

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psorlasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oliponucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Ecytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and arythroleukemia associated with human Zcytor18 splice variant. New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand WVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540 Indels 14; Gaps 107 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNWRFETDYFVRVVPF LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMRAAARPRLCVANEGVGP 181 PSIKNESNYHPFFFRTRACDILLIQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQOENIYSHLDEESSESSTYTAA LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGGRE 121 FLKGFRVILBELKSEGROCOOLILKDPKOLNSSFRRTGMESOPFLNMKFETDYFVKVVPF Query Match 97.8%; Score 3925; DB 23; Length 739; Best Local Similarity 98.1%; Pred. No. 0; Matches 739; Conservative 0; Mismatches 0; Indels 14 Claim 1; Page 102-106; 119pp; English. eg G 26-JUL-2000; 2000US-220747P. Presnell SR, Kuestner RE, N-PSDB; ABA95035, ABA95036. (ZYMO) ZYMOGENETICS INC. WPI; 2002-217048/27 739 AA; Sequence. 167 301 287 361 101 121 181 셤 윱 ð 셤 ö 셤 ö 셤 - 원 ä 8 Ś

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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunosublatory, anti-inflamatory, anti-dabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anci-elsheimer's, renal, asti-parkinsonian, anti-convulsant, anti-elshematic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (ILI7nip) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. hepatitis and obesity), neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin 17; hIL-17 receptor like protein; immunomodulatory; and anti-infifammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexis; cacheris; neuronal dysfunction; lung disease; bone disease; pascular disorder; eye disorder; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
                                                                                                     VLNDVMCKPGPESDFCLKVEAAVIGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660
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                                                                                                                                                                            LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEE 720
                                                                                                                                                                                                 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR
                                                         237. GSRRINTERSKSGRSLYVAICHMEIGFIDEEPDWFEKQFVPPHPPPLRYREPYLEKFDSGL
                                    OGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Interleukin 17 (hIL-17) receptor like protein.
                                                                                                                                                                                                                                             Claim 2; Page 152-154; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                          904 ... AAU09904 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes, psoriasis and glaucoma
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28-NOV-2000; 2000US-0724460.
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consistenction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. cerema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporiosis and hyperaclocemia, vascular disorders (e.g. stroke and atheroscierosis, cancers (e.g. luckemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and misorialise), eye disorders (e.g. infertility and misorialise), eye disorders (e.g. infertility and cetter and misorialise), eye disorders (e.g. disorders (e.g. infertility and cetter and cuntiate the presence of similar nucleic acids in samples and identify pattents needing restorative theirapy. The Inility may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The antic acid sequence of the human contractivity in the mathon acid sequence of the human contractivity. This is the amino acid sequence of the human contractivity in the protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
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                                                                                                                                                                                                                                                                                                                    97.2%; Score 3901; D
97.6%; Pred. No. 0;
ive 1; Mismatches
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                                                                                                                                                                                                                                                                                         Sequence 738 AA;
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707 "PPALPSKILSSGSCKADLGCRSTTDELHAVAP 738
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AAU09953 standard; Protein; 738 RESULT 5

AAU09953;

(first entry) 14-FEB-2002

ophthalmological; Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppessive; anti-microbial; hepatic; anabolic; ancrectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukeamic; anti-infertility; ophthalmologic hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; Human Interleukin 17 (hit-17) receptor like protein substitution #3 mutein.

Homo saptens.

Synthetic:

/label- Ser, Thr, Ala, Cys Location/Qualifiers 363 Misc.difference

WO200168859-A2

20-SEP-2001.

15-MAR-2001; 2001WO-US08678

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC

Jing S;

WPI; 2001-611392/79.

acids encoding interleukin 17 receptor like polypeptides, for preventing, diagnosing and treating, e.g. leukemla, asthma, s; psoriasis and qlaucoma diabetes, psoriasis and glaucoma Nucleto useful

Claim 20; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

Treceptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
tmannosuppressive, hepatic, anabolic, anti-diabetic, anti-microbial,
costeopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
cophthalmological activities. The IL-17 receptor like nucleic acids and
company be used to prevent and treat disease associated with
consider (or example immune disorders (e.g. inflammation, diabetes and
consider (e.g. anorexia, cachexia and obesity), neuronal
cyality disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
cyality disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
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considers (e.g. cystic fibrosis, asthma and emphysema), skin disease
considers (e.g. cystic fibrosis, and hypercalcaemia), wellowed
considers cancer), reproductive disorders (e.g. leukaemia, myeloma and
considers cancer), reproductive disorders (e.g. leukaemia, myeloma
considers (e.g. strucker), and any also used as disquested probes used as
considers needing restorative therapy. The ILIPIIP may also be used as
considered in the production of antibodies against the proteins and in

PPALPSKILSSGSCKADLGCRSTTDELHAVAP

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RESULT 6

AAU09954 standard; Protein; 738 AA.

14-FEB-2002 (first entry)

AAU09954;

BXXXB

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expression and activity.
Wote: This sequence is not given in the specification but is based on the "buman interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 20.
entify modulators of expression and activity. The antibodies and antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                                                                    FIRGPRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKPETDYFVKVVPF 166
                                                                                                                                                                                                                                                                                                                                                            PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240
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                                                                                                                            Query Match 97.1%; Score 3897; DB 22; Best Local Similarity 97.5%; Pred. No. 0; Matches 733; Conservative 1; Mismatches 4;
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Sequence Query Match

738 AA;

97.1%; Score 3896; DB 22; Length 738;

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The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatcory, anti-discheric, anti-nicrobial,
immunosuppressive, hepatic, anbolic, anti-lathamer's renal,
costeopathic, vascular, cytostatic, anti-lathametic, dermatological,
cototians may be used to prevent and treat diseases associated with
cototians may be used to prevent and treat diseases associated with
cototians may be used to prevent and treat diseases associated with
cototians may be used to prevent and treat diseases associated with
cototians rejection), infections (e.g. inflammation, diabetes and
cytostaticals (e.g. dystoins), infections (e.g. inflammation, diabetes and
cytostaticals (e.g. cystofic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasis), kindery disease (e.g. glomerulonephritis),
cototians and psoriasis), kindery disease (e.g. leukemia, myeloma and
cototians and tits complements may also used as disquestic the presence of samilar nucleic acids in samples and identify
cytotiets the presence of samilar nucleic acids in samples and identify
cototiets and antigonists may also be used to down regulate
contigues in the production of antibodies against the proteins and an exprist.
                                                                              Interleukin 17; hii-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonlan; anti-envulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutant;
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Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
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28-NOV-2000; 2000US-0724460.
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-corvulant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer human; mutant;
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llarity 97.5%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunoadulatory, anti-inflammatory, controllar, cytostatic, anti-indexemic, anti-inflammatory and proteins may be used to prevent and treat disease associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammaton, diabetes and transplant respection). Infections (e.g. inflammation, diabetes and transplant respection). Infections (e.g. inflammation, diabetes and dysorders (e.g. anorexta, cacheait and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), weight disorders (e.g. anorexta, asthma and emphysema), skin disease (e.g. stroke and atherosclerosis, cancers (e.g. jufertility and bone diseases (e.g. osteoporosis and hypercalcaemia, mysloma and breast cancer), reproductive disorders (e.g. infertility and miscaritage), eye disorders (e.g. infertility and miscaritage), eye disorders (e.g. infertility and its complements may also used as dispussed to probes to detect and quantitate the presence of similar nucleic acids in samples and identify modulators of samples against the proteins and in assays to identify modulators of empression and activity. The antiques in the production of antibodies against the proteins and in assays to identify modulators of empression and activity. The arrawainn and antivity. The
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Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ASRNSGLINITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.0%; Score 3894; DB 22; Length 738; Best Local Similarity 97.5%; Pred. No. 0; Matches 733; Conservative 1; Mismatches 4; Indels 14.
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                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page :; 158pp; English.
                                                                                                                                                                                                                                                                              15-MAR-2001; 2001WO-US08678.
                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611392/70.
                                                                                                                              Misc-difference 45
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                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-); AMGEN INC
                                                                                                                                                                              WO200168859-A2
                                           Homo saplens.
Synthetic.
                                                                                                                                                                                                                                          20-SEP-2001.
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mutein.
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Interleukin 17; hil.-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; atti-alzhelmer's; atti-parkinsonian; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophihalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; Human Interleukin 17 (hIL-17) receptor like protein substitution #2. /label- Phe, Leu, Val, Ile, Ala, Tyr Location/Qualifiers

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anti-inflammatory; anti-diabetic: immunosuppressive; anti-microbial; hepatis; anabolic; anorectis; anti-alzhelmer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal, osteopathic; vascular; cytostatic; anti-leukemenic; anti-infertility; ophthalmological; hepatitis; anorezia; cachesta; neuconal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL 660
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                                                                                                   LPRERLAPRPRVFLCYSSKDGQNHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE
                                                                                                                                                                                                     WYIOKIHESOFIIVVCSKGMRYFVDRKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ
                                                                                                                                                                                                                                                                                           SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLESRDHGLQEPGQHTR
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28-NOV-2000; 2000US-0724460
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receptor like polypeptides useful as vaccines and in gene therapy. These
have immunoaudulatory, anti-inflammatory anti-diabetic anti-microbial,
they immunosuppressive, hepatic, anabolic, anti-diabetic, anti-microbial,
anti-parkinsonian, anti-convulsant, anti-sthmatic, dermatological,
catepathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
cophthalmological activities The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat disease associated with
cophthalmological activities The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat disease associated with
cophthalmological activities of provents and treat disease associated with
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                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding interleukin 17 recepting 11ke polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
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Pred. No. 0;
!; Mismatches 4; Indels 14.
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                                                                                                                 16-MAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460.
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Best Local Similarity 97.5:
Matches 733; Conservative
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          20-SEP-2001.
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Treceptor like polypeptides useful, as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, and anti-diabetic, anti-diabetic, anti-diabetic, anti-diabetic, anti-diabetic, anti-diabetic, anti-diabetic, ant
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                                                                                                                             receptor like polypeptides,
treating, e.g. leukemia, asthma,
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                                                                                                                             Nucleic acids encoding interleuking 17 useful for preventing, diagnosing and
                                                                                                                                                                                                                                                                  Claim 23; Page -; 158pp; English.
                                                                                                                                                                                                 diabetes, psoriasis and glaucoma
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                                                                                                                                                                                                                                107 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 166
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                                                                                                              1 MAPWILQICSVFFTVNACLINGSQLAVAAGGSGRAWGVDTCGWR------GVGP 46
                            DB 22; Length 738;
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                                           Pred. No. 0;
1; Mismatches
                           97.0%; Score 3894;
97.5%; Pred. No. 0;
                                      Best Local Similarity 97.5%
Matches 733; Conservative
Sequence 738 AA;
                           Query Match
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzahmer's; anti-parkinsonlan; anti-envulant; anti-astimatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
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treating, e.g. leukemia, asthma,
 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 466
                                                                                                                                                                                                                                    disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Interleukin 17 (hIL-17) receptor like protein substitution #5
                                                                                                         VLNDVMCRPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPL
                              481 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR
                                                                                           OGSRRNYFRSKSGRSLYVALCNMHQFIDEEPDWFEKQFVPFHPPPLRTREPVLEKFDSGL
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28-NOV-2000; 2000US-0724460
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Investment of the partice and the partice and the partice and the manner of the partice and the manner of the partice and the partice and the manner of the partice and the proteins may be used to prevent and treat diseases associated with indude, for example immune disorders (e.g. inflammation disbetes and the particular for example immune disorders (e.g. inflammation disbetes and considerable to the particular particular partice and particular (e.g. anorexia, cachexia and obesity), neuronal distinction (e.g., altheriar and obesity), neuronal distinction (e.g., altheriar and obesity), as and epilepsy), but disorders (e.g. ergence for a statement of particular disorders (e.g., stroke and atheroscierosis, asthma and retinity and and the particular disorders (e.g., stroke and atheroscierosis, cancers (e.g., leukemis, myeloma and present cancer), reproductive disorders (e.g. infertility and processing the particular disorders (e.g., stroke and statemoscierosis, cancers (e.g., infermatice probes to detect and quantitate the presence of similar nucleic acids in samples and identify and quantitate the presence of similar nucleic acids in a samples and identity and particular disorders the presence of similar nucleic acids in a samples and identity and the particular particular particular disorders the presence of similar nucleic acids in a samples and identity and the particular disorders the presence of similar nucleic acids in a samples and identity and the particular disorders the presence of similar nucleic acids in a samples and identity and the particular particular disorders the presence of similar nucleic acids in a samples and identity and and an and account the particular disorders the presence of similar nucleic acids in a samples and ident Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22. patients needing restorative therapy. The ILITrip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The invention describes movel nucleic acids encoding interleukin (IE) 8888888888888888888888888888888888

Sequence 738 AA;

241 FRFFYLHIKLKHEGPFKRKTCKQEQTTETTSCLLONVSPGDYIIELVDDFNTTRKVMHYA 300 LKPVHSPWAGPIRAVALTVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAA 360 420 121 FLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF 180 166 WVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQ 480 61 ASRNSGLYNITERYDNCTTYLNPVGRHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120 4; Indels 14; Gaps 1 MAPWIQICSVFFTVNACINGSQLAVAAGGSGRAMGVDTCGWR------GVGP 46 1 MAPWLQLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 107 FLKGFRVILEELKSEGROCQCILKDPKQLNSSFKRTGMESQPFLNNKFETDTFVKVVPF 127 PRFFYLHYKLABGPFKRATCKOBOTTSTLLONVSPGDYIIELVDDTNTTRKVMHYA LPRERLRPRPRVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQRE 481 SSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTR Length 738; Score 3890; DB 22; Pred. No. 0; 1; Mismatches 4; Query Match Best Local Similarity 97.5%; Matches 733; Conservative 347 47 287 307 361 421 467 8 윱 셤 셤 셤 ð a ð 셤 ď 셤 ð ö 셤 å 셤 ö à

541 QGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRIREPVLEKFDSGL 600

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anti-inflammatory; anti-diabetic; imminosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathlic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anoresta; cacheatis; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomedulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-instinantic, dermatological, anti-corvulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor like polypeptides,
treating, e.g. leukemia, asthma,
                                                                                                              LHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGERE 720
                                                                                                                                  Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
                                                                                                                                                                               PPALPSKILSSGSCKADLGCRSTTDELHAVAP 752
                                                                                                                                                                                           707 PPALPSKILSSGSCKADLGCRSTTDELHAVAP 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Cys, Ala, Ser
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602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes, psoriasis and glaucoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000US-189816P
28-NOV-2000; 2000US-0724460
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Synthetic.
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weight disorders (e.g. anorexia, cacheria and obesity), neuronal dysfunction (e.g. Alzaheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. Alzaheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, askima and emphysema), skin disease (e.g. eczema and paoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. oxteoporosis and hypercal camia, wascular disorders (e.g. stroke and atheroscierosis, cancers (e.g. linfertility and breast cancer); reproductive disorders (e.g. linfertility and miscarriage), eye disorders (e.g. glaucomarand retinal neuropathy). The DNA and its complements may also used as disquostic probes to detect and quantitate the presence of similar nucleic acids' in samples and identify particular the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The antibodies and antagonists may also be used as anti-militing antibodies and antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                              Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPWIQLCSVFFTVNACINGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGP 60
     hepatitis and septicaemia),
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                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 738;
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                                                                                                                                                                                                                                                           expression and activity.
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The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; DNAX cytokine receptor subunit 8; DCRSB; phosphate labelling;
gene therapy; protein therapy; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated antigente human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; Length 738;
                                                                                                                                                                                                              Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.
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Pred. No. 0;
2; Mismatches 11; Indels
721 PPALPSKLLSSGSCKADLGCRSTTDELHAVAP 752
                             707 PPALPSKILSSGSCKADIGCRSTTDELHAVAP 738
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Misc-difference 25
                                                                                                                AAU11355 standard; Protein; 738 AA.
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Matches 725; Conservative
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                                                                                                                                                                                                                                                                                                Homo saptens.
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30-DEC-1999;
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   Buman, Interleukin-17 receptor; IL-17RH4; agonist; antagonist;
PRO20036; DNA 154095-2998; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; diabetes mellitus;
allergic disease; asthma; demyelinating disease;
degenerative cartilaginous disorder; transplantation associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRFFILHTELHEGPFRERTCKOEQTTEMTSCLLQNVSPGDIIELVDDTNTTRKVMHTA 285
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19.24
/note- "N-myristoylation site"
31.34
/note- "Asn is N-glycosylated"
38.41
/note- "Asn is N-glycosylated"
56.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Interleukin 17 receptor, IL-17RH4.
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Grimaldi CJ;
Vandlen RL;
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                                                                                                                                                                                                                    312.319 Cote Tyrosine kinase phosphorylation site
                                                                                                                                                                                                                                                                                                         Tyrosine kinase phosphorylation site
                                                                                            233..235
/note= "cAMP/GMP-dependent protein kinase phosphorylation site"
256..269
/note= "Asn is N-glycosylated"
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L, Li H, Hillan KJ, Tumas D, Van Lookeren M,
CK, Williams PM, Wood WI, Yansura DG;
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/note= "N-
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/note= "Ty
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113..116
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707..71
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N-PSDB; AAS09517.
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The sequence is PRO20026 which is the human Interleukin 17 receptor, II-77RH4, encoded by DNA 154095-2998. A composition containing ant/agonists to the PRO polypeptides or individual components containing ant/agonists to the PRO polypeptides or individual components occidentains of teating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, dispathic inflammatory myopathy, sjoaren's syndrome, systemic sclerosis, an idopathic inflammatory myopathy, sjoaren's syndrome, systemic vasculitis, sacrodated disbase, an autoimmune haemolytic ancents, untuoimmune the contact demanitis, an allosing mellitus, immune-mediated skin disbase, on chard femanitis, an allosing collassase or food disbase, contact demanitis, an allosing collassase or food disbase, on this ammatory demyelinating polymeuropathy. Treating a prolosi charanterious disorder comprised administering a prolosi contact demanitation associated disease, or a chronic inflammatory demyelinating polymeuropathy. Treating a prolosi contact demyeliate administ comprised administering a prolosi contact demyeliate administ an entragemental companies. Or antagonist, or antagonist to the mammal. Numerous contact demyeliate administration associated diseases. 42 RMKAAARPRICVANE-GVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQY 100 101 ACHDOVAVTILWSPGALGIEFLKGFRVILEELKSEGROCOOLIIADPROLNSSFKRTGME 160 Gaps 62 RASASGVPALFVSGEOGVGPASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQY 8; Indels 14; 92.3%; Score 3703; DB.22; Length 728; 96.7%; Pred. No. 0; tive 2; Mismatches 8; Indels 14; Conservative Mest Local Similarity
Matches 702, Conserva-728 AA; . Ouery Match Sequence

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143 EMISCLLQNVSPGDYIIELVDDTNTTRVWHYALKPVHSPWAGPIRAVAITVPLVVISAF 302 267 ETTSCLIQUVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327 ATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV 387 NYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD 507 LSTRYRLADNI.PQI.CSHI.HSRDHGI.QEPGQHTRQGSRRNYFRSKSGRSLIVAICNAHQFI 567 GPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSE 687 221 ISQ ------HGSDMQVSFDHAPHNFGFRFFTLHYKLKHEGPFKRKTCKQEQTT 483 **368 423** 543 328 303 ¥ 208 268 628 ð 8 õ a ð, 셤 ઠે 음 Š 셤 à 셤 ö 셤 ð 용 Š g Š 윱 õ

HAVAPL 728 723 AAU10602 **X B X B X B X**

RESULT

AAU10602 standard; Protein; 739 AA.

AAU10602;

14-FEB-2002 (first entry)

Human interleukin 17 (hIL-1) receptor-like protein version 2.

Interleukin 17; hil.-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetto; immunosuppressive; anti-inframmatory; anti-diabetto; immunosuppressive; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; anti-convulsant; anti-infertility; ophthalmological; vascular; cytostatic; anti-inferminonal dysfunction; lung disease; hepatitis; anorexia; cachexia; neuronal dysfunction; lung dis bone disease; vascular disorder; eye disorder; cancer; human

Homo sapiens.

#0200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US08678

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC

Jing S;

WPI; 2001-611392/70: N-PSDB; AAS16201. Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukaemia, asthma, diabetes, psoriasis and glaucoma

Claim 2; Fig 1; 158pp; English.

The Invention describes novel nucleic acids encoding interleukin (IL) 17

Treeptor like polypeptides useful as vaccines and in gene therapy. These

CC receptor like polypeptides useful as vaccines and in gene therapy. These

CC mave immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,

anti-parkinsonian, anti-corvulant, anti-asthmatic, dermatological,

anti-parkinsonian, anti-corvulant, anti-asthmatic, dermatological,

CC descopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and

CC proteins may be used to prevent and treat diseases associated with

CC proteins may be used to prevent and treat diseases associated with

CC proteins may be used to prevent and treat diseases associated with

CC transplant rejection, infections (e.g. inflammation, diabetes and

CL transplant rejection), infections (e.g. inflammation, diabetes and

CL transplant rejection), infections (e.g. inflammation, diabetes and

CL transplant rejection), infections (e.g. inferious), sitseamed and

CC transplant rejection, infections (e.g. inferiilty), neuropally,

CC dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),

CC dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),

CC dysfunction (e.g. Alzheimer's and hypercalcaemia, weelong and

CC bone diseases (e.g. osteoporosis and hypercalcaemia, weelong and

CC bone diseases (e.g. osteoporosis and hypercalcaemia, weelong

CC on diseases (e.g. osteoporosis and hypercalcaemia, weelong

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                                                                                                                                                                                                                                                                                                 123 KGFRVILEELKSEGRQCQQLILKDPRQLNSSFKRTGNESQPFLAWKFETDYFVKVVPFPS 182
                                                                                                                                                                                                                       109 KGFRVILEELKSBGRQCQQLILKDPRQLNSSFRRTGWBSQPPLNWKPETDYFVRVVPPPS 168
                                                                                                                                                                                                                                                      183 IKNESNYHPPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFR 242
                                                                                                                                                                                                                                                                    PVHSPWAGPIRAVAITVPLVVISAFATLPTVMCRKKQQENIYSHLDEESSESSTYTAALP 362
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                                                                                                                                                             RNSGLYNITERYDNCTTYLNPVGKHVIADAQNITISQYA@HOQVAVTILMSPGALGIEFL 122
                                                                                             Gaps
                                                                                                               3 PWLOLCSVFFTVNACLNGSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGPAS 62
                                                                                                                                9 PGSQQC------CLHIDSMGICVG------RANWIASASCS---LVFPQGVGPAS 48
           sequence shown in AAU10601 which is incomplete in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVL
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                                                                                           20;
                                                                     Length 739;
                                                                 Query Match 92.3%; Score 3703; DB 22; Length 7: Best Local Similarity 93.7%; Pred. No. 0; Matches 704; Conservative 5; Mismatches 22; Indels
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the invention.
Note: Residues 1-288 of this sequence
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                                             Sequence 739 AA;
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The invention relates to an isolated cytokine receptor polypeptide designated Ecytori8. The Ecytori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Ecytori8 in vivo by gene therapy techniques. Ecytori8 oilgonucleotide probes are useful for in vivo diagnosis, and the Ecytori8 probes and primers can be used to detect and localize Ecytori8 gene expression in tissue samples. The probes are also useful for in cetetching gross aberrations in chromosome 3 in which Ecytori8 gene resides. The Ecytori8 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine Ecytori8 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                    New cytokine receptor polypeptide designated zcytori8, useful for initialiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand
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             ir proteinosis; familial periodic fever;
chromosome 3p14.3; gene therapy; mouse.
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                                                                                                                                                                 23-JUL-2001; 2001WO-US23253
                                                                                                                                                                                             26-JUL-2000; 2000US-220747P
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                                                                                                                                                                                                                                                                                                 WPI; 2002-217048/27.
N-PSDB; ABA95037, ABA95038.
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Best Local Similarity 85.2%
Matches 645; Conservative
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              pulmonary alveola
erythroleukemia;
                                                                                              WO200208259-A2.
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PPSIKNESNYHPFFPRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNF GFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHY

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300 ALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIISHLDEESSESSTITA 359

SLCREGOR 419 	AEKLRQAK 479 AEKLRQAK 466	LQEP-GQH 538 EQEVIGQH 523	PVLEKFDS 598 PVLEKFDS 583	PALDGSAA 656 : : : PSCDSAPA 643	SVSSSSGL 716 	
360 ALPRERLRPRYFLCYSSKDGONHANVYQCPAYFLQDFCGCEVALDLWEDFSLCRBGQR 	EWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAK 	QSSSAALSEFIAVYEDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEP-GQH 	539 TROCSRRNYFRSKSGRSLYVALCNMHQFIDEEDDWFEKQFYPFHPPPLRYREPVLEKFDS	599 GLVLNDVAKCREQPESDFCLKVEAAVLGATGPADSQHESQHGCLDQDGEARPALDGSAA 	LQPLIHATVKAGSBSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGL 	SYTDELHAVAPL 753 : : SHTDELQALAPL 739
ALPRERIRPRPKVFLCYSKDGONH 	EWVIQKIHESQFIIVVCSKGMKYFV 	QSSSAALSKFIAVYFDYSCEGDVPG 	TROGSRRNTFRSKSGRSLIVVALCHM 	GLVLNDVMCKPGPESDFCLKVEAAV 	LQPLLHTVKAGSPSDMPRDSGIYDS 	GEEEPPALPSKILSSGSCKADIGCRSYIDELHAVAPL 753 : : :
360	420	480	539	599	644	717
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Search completed: May 19, 2003, 09:20:05 Job time : 59.6401 secs

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2626.495 Million cell updates/sec
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1100%
Listing first 45 summaries
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1j9 brachydanio 1j6 brachydanio 54 caenorhabdi 50 homo sapien 19 homo sapien Ogufa0 homo saplen Description Q8qhj6 Q9na64 Q9h460 Q96kn9 SUMMARIES A Length DB Query Match

Result

09qzp6 mus musculu 013399 ustilago ma Q24573 drosophila 054978 mus musculu 096687 homo sapien 099pv2 rattus norv

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09ay10 oryza sativ 088737 mus musculu

09bhw7 leishmania 09n918 leishmania 08rcu4 homo sapten 09n0b3 macaca fasc 09v490 drosophila 09v490 drosophila 09v490 drosophila 09y216 homo sapten 09lyd arabidopsis 09lyd bomo sapten 09lyd bomo sapten 09lyd drosophila 09lyd drosophila 09lyd drosophila 09lyd mus musculu 09lat qallus qallus qallus qallus qallus doboo sapten 09liza arabidopsis 09lyd mus musculu 09lat qallus qallus qallus qallus homo sapten 09lkis homo sapten 09lkis homo sapten 09lkis homo sapten 01517 homo sapten 01517 homo sapten 01517 homo sapten	ta; Eureleostom1; dag: Homo. Gassenhuber J., tabases. CRC64; Length 564; indels 0; Gaps 0; indels 0; indel
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181 DNLPQLCSHLASRDHGLQEPGOHTRQGSRRNYFRSKSGRSLIVAICNNHQFIDEEPDWFE 240
           241 KQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300
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                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxiD=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.2%; Score 1817.5; DB 11; Length 582;
83.4%; Pred. No. 8e-148;
ive 25; Mismatches 38; Indels 7;
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Furthauer M., Lin W., Ang.S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPR-mediated FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 AA; 65263 MW; 56663B2981C4268E CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar expression to RGF protein (Fragment).
                                                                                                                                                                                                                     PRT; 582 AA.
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Nat. Cell Biol. 4:170-174(2002).
EMBL; AF424804; AAL79530.1;
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Matches 351; Conservative
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Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID-7955;
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MEDITHE-11812436; Pubmed-11802164;
MEDITHE-2182436; P. Kudoh T., Dawid I.;
Friesel R., Kudoh T., Dawid I.;
"Identification of Sef, a novel modulator of FGF signalling.";
Nat. Cell-Blol. 4:165-169(2002).
BENBL: AF364103; AAL76112.1; *
SEQUENCE 745 AA; 83431 MW; 56FEIFOB9D98DDB4 CRC64;
                                                                                                                                                                                           01-UUN-2002 (TIEMBLEEL. 21, Created)
01-JUN-2002 (TIEMBLEEL. 21, Last sequence update)
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556 ------EPAIERITGRND------VIFDMQCELALQHPCVISCHFSYIN 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DFCGCEVALDLWEDPSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 DVFNLNVHLDVWDEDDI-EENRAETINSSIVRANKVIIINSIG-AFF--RTVFRHQR--- 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 -----RLMD-NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 MHQPIDEEPDWFEK-----EP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 KLNYIESDPOWFENTHHRVATRRVSELEAHNIVPL-PPSLEVRVEDEDAFGOMETLPIDE 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 VLEKF-------DSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             706 LKEKFAARRDLEVEVLDSEDVKLLEDVKCAPGP----IHVEPTEPEVLEPAEEPMEEAE 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKQQENIYSHIDEESSESSTYTAALPREKLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 GGLDQDGEARPALDGSAA----LQPLL-HTVKAGSPSDWPRDSGIYDSS-VPSSELS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 6:8%; Score 150.5; DB 5; Length 846; Best Local Similarity 22.5%; Pred. No. 0.00035; Matches 94; Conservative 57; Mismatches 147; Indels 119;
                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for investigating blology"; Science 882:2012-2018(1988), EMBI, ALIIOS. CABS-470.1; SEQUENCE 846 AA; 94852 MW; 613AEF55EBB89EA4 CRC64;
                               Ainscough R.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 111.5;
                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00037; CNX; 1.
PROSITE; PS00407; CONNEXINS_1; 1.
PROSITE; PS00408; CONNEXINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL121749; CAC10186.1; -.
InterPro; IPR00500; Connexin.
Pfam; PF00029; connexin; 1.
SMART; SM00037; CNN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                094460;
01-MAR-2001 (
01-MAR-2001 (
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SEQUENCE
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                                                                                                                                                                                                                                       none;
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09H460
                                    ST TE DE DE DE LE PER RESCO COSTO DE LA PERSONA DE LA PERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 RKKQOENIYSHLDEESSESSOTTALSADRPWPRPRIFICTSSRDGAKHLAVIQSFAFFL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ODFCGCEVALDIMEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 R-----GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 ILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVALCNNH 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 QFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 -----GATGPADSQHESQHGGIDQDGEARPAIDGSAAIQPLIHTVKAGSPSDMPRDSG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 ILPQTPQVGVSLSLSREDLGEGSSSQD------AGSCRPVLHTDGSASPPEMPRDSG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYDSSVPSSELSLPLAMEGISTDQTETSSLTESVSSSGLGEEEPPALPSKILSSGS-CKA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RKKOGENITSHLDEESSESSTYTAALPREKLRPRFKVFLCYSSKDGQNHMNVVQCFAYFL 60
                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Bikaryota, Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio
NCBI TaxiD-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
48.2%; Score 1065.5; DB 13; Length 745;
Best Local Similarity 52.6%; Pred. No. 5.6e-83;
Matches 222; Conservative 63; Mismatches 104; Indels 33;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-21824237; PubMed-11802165;
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuerthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, ARA0123, ALT/8817 1; SEQUENCE 745 AA. 83437 MW; 75BB9EDCC08A4652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TERMELTE1. 15, Created)
01-OCT-2000 (TERMELTE1. 15, Last sequence update)
01-DEC-2001 (TERMELTE1. 19, Last annotation update)
164G10A.6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signaling antagonist Sef.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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DL .728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signalling.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heath P.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 AA; 37805 MW; 07EB6478067F8995 CRC64;
                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) BA425A6.2 (Similar to connexin) (Fragment).
PRT; 348 AA
                                                                         (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequ
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Wiemann S., Well B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W.; Boecher H., Bauersachs S., Blum H., Lauber J., Decher M., Bloccher H., Bauersachs S., Blum H., Mewes H.W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of: 500 Novel Complete Protein Coding Human CDNAs.; EMBL; AL117401; CAB55902.2;
                                                                                                                                                                                         Hypothetical protein.
SEQUENCE ... 428 AA; 45443 MW; FA75BACIA3FDB3EE CRC64;
                                       MEDLINE-21154917; PubMed-11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative gag-pol polyprotein.
                                                                                                                                                                                                                                                     Best Local Similarity 23.5%;
Matches .. 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL; AC074283; AAK02020.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyprotein.
SEQUENCE 10
                                                                                                                                                                                                                                         Query. Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q9AYIO;
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                                                                265 LVLNDVMC-----RPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 316
                                                                                                      317 DGSAALQPLLHTVRAGSPSDMPRDSGIYDSSVP---SSELSLPLMEGLSTDQTETSSLTE 373
                                                                                                                              265 LVLNDVNC-----KPGPESDFCLKVEAAVLGATGPADSQHESGRGGLDQDGEARPAL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 DGSAALQPILHTVKAGSPSDMPRDSGIYDSSVP---SSELSLPLAMBGLSTDQTETSSLTE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Elberger J., Soehl G., Willecke K.;
"Structural and functional diversity of connexin genes in the mouse
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 111.5; DB 4; Length 370; 28.9%; Pred. No. 0.26; Live 25; Mismatches 56; Indels 25
28.9%; Pred. No. 0.24;
tive 25; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and human genome.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ414554; CAC93466.1;
EMBL: AJ414554; CAC93466.1;
Pfam; PF00029; Connexin;
PROSITE; PS00407; CONNEXINS.1;
PROSITE; PS00407; CONNEXINS.2; UNINGWN.1.
SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;
                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Conestia(0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC_2001 (TrEMBLrel. 15, Last annotation update)
Bypothetical 45.4 kDa protein.
DRF2204342311.
                                                                                                                                                                                                                                                                    PRELIMINARY; PRT; 370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 AA
                                                                                                                                                                                        396 AADDPRGSGSEEQPSAAPSRLAAPPSCSS 324
                                                                                                                                                                     374 SVSSSGLG-EEPPALPSKILSSGSCKA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 SVSSSGLG-EEPPALPSKLLSSGSCKA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 Best Local Similarity, 28.9
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Watches
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17;
                                                                                                                                                                 186 ICSHIHSRDHGIQE--PGQHTRQGSRRNTFRSKSGRSLIVAICNMHQFIDEEPDWFEKQF 243
                                                                                                                                                                                                                                                                                                       163 AVSSGHIQCEKAADIAPGGILT--LRNDSSISEASRP-----STHKF-----PLLPRRG 210
                                                                                                                       139 KIRQAKQSS-SAALSKFIAVYFDYSCEGDVPGI------LDLSTKYRLMDNIPQ 185
                                                                                                                                                                                                                                                                                                                                                                                    244 VPFH-PPPL------RYREPVLEKFDSGLVLNDVM----CRPGPESDFCLKVEAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 VIGATG-PADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVRAGSPSDMP-----RD 340
                                                                  78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 EPLMLPPPLELGYRVTVEDLDREKEAAFQRINSALQVEDKAISDCRPSRPSH---TLSSL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 ATGASGLPAVSKAPS----MDAQQETHKSQDCLGLLDPLASA--AGVPSTAPMSGKKHRP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --YFDYSCEGDVPGILD-LSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNY-- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKGGGRGSGKGELFLVAVSALAEKL------157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 SG-IYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza astiva (Rice)
Bukaryock; Viraliplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
Kim H.-R., Rambo T., Henry D., Simmons J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 4.9%; Score 108; DB 10; Length 1058; Local Similarity 22.1%; Pred. No. 2.2; les 85; Conservative 52; Mismatches 131; Indels 116;
5.0%; Score 110; DB 4; Length 428;
23.5%; Pred. No. 0.42;
Ive 42; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1058. AA; 115228 MW; 9E39B2C564FC6CE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
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01-JUN-2002 (TIEMBLRel. 21, Last sequence update)
01-JUN-2002 (TIEMBLRel. 21, Last annotation update)
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đ	SECTION 1 :	Db 3692 PQASPAPAM	POASPAPAMOKKGOPGYPSSADYSOSSRAPS
ð		QY 330 KAGSPSDMP Db 3752 AQPQNGGRQ	330 KAGSPSDNPRDSGITDSSVPSSELSLPLARG
a	-QCAFLGYSTLHKGFKCLDISTGRVYISRDV-VFDEQIYPFANLHPNAGAR	Oy 390 PSK 392	
දු සි	23. KERYLL. ERLD SGLYMONINGER 1 1 1 1 1 1 1 1 1 1	1 : 0b 3809 PSQ 3811	
Š.	286 AAVLGATGB332	RESULT 11 0902P6	· · · · · · · · · · · · · · · · · · ·
윰	PERGESGSGGHTGSHPEDDALAASDASVAESGNDTGT	9QZP6; 9QZP6;	
<u>8</u> 8	333 SPRINGROSG-ITDSSYPSSELSLPLARGLSTDOTFISSITESYSSSGL-; -GREEPP 387 [1] [2000	(TrEMBLrel, 13, Created) (TrEMBLrel, 13, Last seq (TrEMBLrel, 21, Last ann
. 8	388 AL-PSKILSSGSCKADLGCRSTTD 410	DE Neuronal IL-16. GN IL16.	
a .	541 MLGPATRSRHGIRKPKKYTD 560	Eukaryota; Mammalia;	.us (mouse). .Metazoa; Chordata; Crania Eutheria; Rodentia; Sciuro
RESUL O8873	I 10 ·	NCBI_TaxII [1]	
3 A 2	088737. PRELIMINARY; PRT; 3942 AA. 088737;	RA Kurscher From N.A. RA Kurscher C., Yuzaki M.; PH "Mantonal interlemble-16	N.A. Yuzaki M.; orlembin-16 (NII16): m
គ គ	1998 (TrEMBLrel. 08, Created) 1998 (TrEMBLrel. 08, Last sequence up	pr.	. (27 711)
	rel. 19, Last	E SE	BL; AF175292; AAD55393.1; SP; Q14005; 1116.
	Chordata:	InterPro;	17/0535; 1110. IPR001478; PDZ.
	Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinus.	ığ.	M00228; PDZ; 4. PS50106; PDZ; 4.
	(1) SEQUENCE FROM N.A.	SEQUENCE	141434
	AEDINE-123 S.V. Bunmartt-Vila L., Languaese K., Richter K., Kindler S.,	Query March Best Local Similarity Matches 71; Conser	4.8%; Score 1 larity 22.5%; Pred. N Conservative 29; Mism
	malla K.H., Kampf U., Franzer J.T., Stum finger E.D.;	Oy 138 EKLROAKOS	LSKFIAVYFDYSCE
	"Bassoon, a novel ginc-finger CAG/Glutamine-repeat protein selectively localized at the active gone of presynaptic nerve terminals.";	282	
	200	Оу 191	- HSRDHGLØEPGQHTRØGSRRNY
	598.1; 598.1;	Db 318 LSSSTCGAQ	LSSSTCGAQDSSPFSLESPAS-PASTAKPNY
2 2 S	ENGL: X17038; CAA76598.1; JOINED. MGD; MGI:127755; BSG. SENTENCE 3042 as 418730 MW: 150267562664886 COCK4.	OY 235 EPDWFEKQFVPFHPP	EPDWFEKOFVPFHPPPLRYREPV
~	4.9%; Score 107.5; DB 11;	277	ESDFCLKVEAAVLGATGPA
Wat Wat	Similarity 19.1%; 8; Conservative 29	432	INSRHPDPQVSEQQLKEAVAQAVEGVKFGR
, O,	181 DNLPQLCSHLASRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNWHQFIDEE 235	Oy 323 OPLIHTVKA	OPLINITYKAGSPSDMPRDSGIYDSSVPSSEL
셤.	3535 DICPOPCSSHSMPDVQEHVRDGPRAHAYRREEGIMLADSHCVVSDSEAYHLGQEE 3589	Db 491KR	KHSAPPHRRAQKIMVRSSSDSSYN
g 4	236 POWPERQPVPFHPPPLRYREPVLEKFDSGLVIANDVACKPG 275	Oy 378 SSGLGEEEPPALPSK : : : : : : :	PPALPSK 392 : : :PGVPSR 558
ð,	276 PESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARP- 314	RESULT 12	
셤	3644 PGRHTSAKEHRHHSDBGRHSGRHAGEEPGRRAAKPHARDMGRHEARPH 3691		PRELIMINARY; PRT;
ď	e e	013399; 01-JAN-1998	05, CI
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107; DB 11; Length 1322;
No. 3.6;
smatches 117; Indels 98; Gaps 13;
SAYHHASESKKGSRQAHTGPSALQPKADTQ 3751
                                  SCLSTDOTETSSLTESVSSSGLGEEEPPAL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WI-----FRSKSGRSLIVAICNMHOFIDE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :| i | i | TNSGSPGGSPCSAGAEPQPSEREGSTHSPSL 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLS----LPLMEGLSTDQTETSSLTESVSS 377
                                                                                                                                                                                                                              iata; Vertebrata; Euteleostomi;
rognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                a dual function PDZ domain
                                                                                                                                                                                                                                                                                                                                                                                                              DB94003A5DCB738 CRC64;
                                                                                                                                                                          equence update)
nnotation update)
                                                                                                                                            1322 AA.
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[1]
SEGUENCE FROM N.A.
MEDLINE-96154192; PubMed-8563758;
Kuroiwa Y., Kaneko-Ishino T., Kagitani F., Kohda T., Li L.L., Tada M.,
Suzuki R., Yokoyama M., Shiroishi T., Wakana S., Barton S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLWEDFSL--CREG-----QREW--VIQKIHESQFI----IVVCSKGMKYF----VDK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 4.8%; Score 105; DB 5; Length 901;
Similarity 20.4%; Pred. No. 3.2;
16; Conservative 56; Mismatches 157; Indels 162; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 KNLSTPAELQAAIDGNRREGRRSSYGQYEAMHNOMPWTPISRPSLPGGMQQMSPLALVTH 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GGMPPYLGGNHPRQQHSQQQQQQHHPQQQQQQQQQHLLQQQRQRSQSPDLSKHEALSA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SGLVLNDVMCRPGPESDFCLKVE--AAVLGATGPADSQHESQHGGLDQDG 310
                                                                                                                                      MEDLINE-90182081; PubMed-8622680; Gregory S.L., Kortschak R.D., Kallonis B., Saint R.; Gregory S.L., Kortschak R.D., Kallonis B., Saint R.; Characterization of the dead ringer gene identifies a novel, highly conserved family of sequence-specific DNA-binding proteins."; Mol: Cell. Biol. 16:792-799(1996). EMBL; 062542; AMB05771.1; TRANSFAC: T04679; -: FlyBase; FBgn0004795; retn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 SAIAEKLR-QARQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLC---- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 -----SHLHSRDHGLQEPGQH----TRQGSRRNYFRSKSGR-----SL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 IVAICHMHQ------FIDEEPDWFEKQFVPFHPPPL-----RIREPVLEKFD---- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 QVALWHMYHNNNSPPGSAHTSPQQREALNLSDSPPNLTNIKREREREPTPEPVDQDDKFV 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         608 DOPPPAKRVGSGLL-----PPGFPANFTLNPHNMAAVAAAG---FHHPSMGHQQDAAS 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARPALDGSAALQPLLHTVKAGSPSDMPRDSGITDSSVPSSEESLFTMEG **** 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostoml;
Mammalla; Eutherla; Rodentla; Sclurognathl; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDE 411
                                                                                                                                                                                                                                                                                                                                                                                            3HT; 1.
96018 MW; 77200EC3601F7B8E CRC64;
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Last annotation update)
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Pfam; PF01388; ARID; 1.
SMART; SM00501; BRIGHT; 1.
SEQUENCE 901 AA; 96018 1
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Matches 96; Conservative
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                                                                                                                  SEQUENCE FROM N.A.
                                                                    NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
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                   SO DE RESERVACION DE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 HVRDVETGTVWLTATLPPIFEDAFISHNKLTKPLIVRESTNRSNLCTSVRTAEHRMSGWT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KNYKHKGGGRGS------GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 EMLGCAAYSSESGSEADKAAIIQDWICGKGSPVIVATSA-------LG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RLMDNLPQLCSHLHS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 VGFDYPHVRFVIHLLGPDLLTDFSQESGRAGRDGMPAESILLAGPQLDDRAP-ASGKASS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AEKGKVAPG---ADKEAMOLYRSRK---YCLRGVLSQLLDQRSDW------ 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 YREPVLEKFDSGLVLADVMCKPGPESDFCLKVEAAVLGATGPADSQH----ESQHGGLDQD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 -----RWCMEGDQLCSVCPGHHF-----QARGPGDQFHFTAPAQAGDPSTQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 GEARPALDGSAALOPLLHTVKAGSPSDMPRDSGIYDSSVPSSE-LSLPIMEGLSTDQTET 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 CF-AYFLODFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIVVCSKGMKYFVDK-- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 RDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQF1DEEPDWFERQFVPFHPPPLR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLDEESSESSTYTAALP-----RERLRPRPKVF------LCYSSKDGONHMVVQ 54
                                                                                                                                                                                                                                                                            Sanchez-Alonso P., Guzman P.;

*Organization.of chromosome ends.in Ustilago maydis: recQ-like helicase motifs at telomeric regions.;

EMBL: AF030885; AAB95264.1;

InterPro: IPR001410; DEAD.

InterPro: IPR00155; Helicase_C.

Pfam; PF00270; DEAD; 1.

Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Mismatches 147; Indels 166;
                                                                                                                                   Eukaryota, Fungl. Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBL_TaxID-5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TERRILAEL: 01, Last sequence update)
01-DEC-2001 (TERRILAEL: 01, Last annotation update)
01-DEC RINGER.
RETN OR DEAD RINGER OR CG5403.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 105; DB 3; Length 757;
20.6%; Pred. No. 2.5;
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01-JAN 1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                         Telomere-associated reco-like helicase (Fragment).
                                                                                                                                                                                    Frankling Com
                                                                                                                                                                                                                                                . . . . . .
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                                                                                                                                                                                                                                              489 SS-HPSINGSGORRKQQPDPPSE 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 VYFDYSCEGDVPGIL--DLSTKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 SSLTESVSSS---SGLGEERPPALPSK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Created)
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                                                                                                     Ustilago maydis (Smut fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Helicase
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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024573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 105; DB 11; Length 1571;
19.2%; Pred. No. 6.8;
tive 49; Mismatches 135; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 DIMEDPSIC----REGOREMVIORIHESQFIIVVCSKGMKYFVDKKNYK--HKGGGRGSGK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 -----SRNCEETFVPSOSLRRROKTTREKLFDFNNARDA------LMGN--- 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 SOKSHTITRPPENKDDDKPFTISVPNDKLKLPIMENGSQGKSC---ERSVIHSIGSAEA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LCSHLHSRDHGLQEPGQHTRQGSRRNTFRSKSGRSLIVAICNMHQFIDEEPDWFEKQFVP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 ------SDSSEHOKNRSRRNFFEGRG------FEKPFVE 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 QHESQHGGLDQDGEARP-------ALDGSAALQPLHTVKAGS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 Q--KSHGGL---GFSKPRPVARSSTQSSSSIYYPRAHSGGNTYEGKEYKDSIIHSLPAPR 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 P-----SDMPRDSGIYDSSVPSSELSLPLAMGGLSTDQTETSSLFESVSSSGLG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 FHPPPLRYREPVLEKFDSGLVL----NDVMCKP----GPESDFCLKVEAAVLGATGPADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogal T., Ota T., Hayashl K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Tamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                encodes for a zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADINALINA (NEW 1992) 216 C2H2.

PRIME PRO0006; zf-C2H2. 11.

PRIMES PRO0006; zf-C2H2. 11.

PROSITE; PSO0025; zn-C2H2; zn-C2H2. 11.

PROSITE; PSO0157; zn-C2H2; zn-CHCER. C2H2_1; zn-C2H2; zn-C2H2. zn-C2
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01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLI1496 fis, clone NT2RP4001235.
BODO saplens (Hunan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
shino F., Surani M.A.;
Peg3 imprinted gene on proximal chromosome 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707 AA
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            785 --EPPSLSGE---SHDSKQDV 800
                                                                                finger protein.";
Mat. Genet. 12:186-190(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 19.2%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4GD; MGI:104748;
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity 19.6%; Pred. No. 2.5;
Matches 107; Conservative 61; Mismatches 180; Indels 197; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      58 YFLQDFCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYK-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 CFNCGSEEROMKDCPMPRNAARISEKRRETMDACGEANNONFOORTHAEEVERFGRFKF 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 -----HSRDHGLOEPGOHTROGSRRNIFRSKSGRSLIVAICNMHOFIDEEPDWFEKQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 LPPDTPPLPRGTPP-----PVFTPPLPKGTPPLT------PSDSPGTRT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 QHGGLDQDGEARPALDGS-----RALQPLLHTVKAGSPSDWPRDSGITDSSVPSS----E 352
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Masuho Y., Kanehori K.;
*NEOO human cDNA sequencing project.*;
*Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AK027702; BAB55308.1;
*InterPro; IPRO018708; Enf_CCRC.
Pfam; PF00098; zf-CCRC; 1.
*SEQUENCE 707 AA; 78475 MW; ED4E954E42672F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 19, 2003, 09:24:00 Job time : 38.7919 secs
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OM protein - protein search, using sw.model - 1808 728
Run on: May 19, 2003, 09:16:08; Search time 27,7988 Seconds (without alignments)
Title: 5.55 US-09-912-157-2 Parfect Rone 4013
Sequence: 31 NAPWIQLCSYPETYNACLNGCRADLGCRSYTDELHAVAPL.753
Scoring, table: Babos 10.0 , Gapext 0.5
Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir4:*

Post-processing: Minimum Match 108 Maximum Match 1008 Listing first 45 s

Database :.

		٠.			SUMMERTES	
Result No.	Score	Ouery	Length	DB	ΙD	Description
-	3005	74.9	564	~	T42695 "	hypothetical prote
	170.5	7	846	~	T27282	
m	126.5	3.5	718	~	T30113	_
*	117	5.3	757	~	T09081	ŏ
S	117	6	917	~	T04661	hypothetical prote
•	. 117	5.3	2946	~	T00867	-
£	116.5	6.7	901	ä	F83781	transposase (08) /
æ	115.5	2.9	938	~	149071	protein kinase - m
ό	115	2.9	966	~	S37627	protein-tyrosine k
. 10	110	2.7.	535	Ċ	- T17212	hypothetical prote
11	110	2.7	. 592	7	149239	vesicle transport
12	108.5	2.7	3788	ď	T13960 .	beige protein homo
13	107.5	2.7	3942	7	T42730	Bassoon protein -
14	107	2.7	3788	~	T30851 .	lysosomal traffick
15	106.5	2.7	638	~	D86477	protein F1504.27 [
. 16	106	5.6	1448	ď	A12007	Subtilase family p
17	105	2.6	. 901	7	JC6093	dead ringer nuclea
18	105	5.6	1571	Ċ	T14155	zinc finger protei
19	104	5:6	1462		B36182	protein-tyrosine-p
8	103.5	5.6	663	~	A39897	GTPase-activating
21	103.5	5.6	930	ď	A84668	Argonaute (AGO1)-1
22	102	2.5	813	N	B47485	ABR protein 2 - hu
23	102	2.5	. 859,	7	A49307	98K GTPase-activat
7	101.5	2.5	822	ď	A47485	ABR protein 1 - hu
25	101.5	2.5	1639	'n	T50119	probable sensory t
36	101	2.5	641	ď	T05497	-
27	101	2.5	664	C	T51247	ARR2 protein [impo
78	101	2.5	1275	ď	A38985	nucleotide exchang
53	100.5	2,5	938	ď	T05533	hypothetical prote

IAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFR 549

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QFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKF

SKSGRSLYVAICHMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKP 609

610 GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGËARPALDGSAALQPLLHTVKAGSP 669

61 LKHEGPPRRKTCKQEQTTEMTSCLLQNVSPGDXIIELVDDTNTTRKVMHYALKPVHSPMA 120

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Db : 421 GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSP '480	DD 704 DELKEKFAAKR
OY *-670 SDMPRDSGIYDSSVPSSELSLPLMARGLSTDQTETSSLTRESVSSSGLGEBEPPALPSKLL 729 ***	Oy 637 OHGGLDQDGEA
Db 481 SDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLL 540	Db 759 AEED-EEDEDD
Db 1541 SSGSCRADIGCRSYTDELHAVAPD: 564	RESULT 3 T30113
The second secon	hypothetical protein
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hypothetical protein 164G10A.e - Caenorhabditis elégans	R; Chissoe, S; Wilson
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change_20-Jun-2000	submitted to the EMBL A;Description: The see
C; Accession: 127282 R; Ainscough, R.	A. Accession . #30113
Submitted to the EMBL Data Library, September 1999	A: Status: preliminary
A/Accession: 127282	A; Residues: 1-718 <ch< td=""></ch<>
A Molecule type: DNA	A; Cross-references; E C; Genetics;
A)Residues: 1-846 <wil> A)Cross-references: EMBL:A110498; PIDN:CAB54470.1; CESP:I64G10A.e</wil>	A; Gene: CESP: F56D1.2 A; Introns: 93/1; 121/
CyGenetics: croud reaction	C; Superfamily: Caenor
A:Gene: CESP:Y64G10A.e A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3 C:Superfamily: Caenorhabditis elegans, hypothetical protein Y64G10A.e	Query Match Smilarion Best Local Similarion Matches 82; Cons
Query Match 4.2%; Score 170.5; DB 2; Length 846; Best Local Similarity 21.4%; Pred No. 3.38-05;	Qy 363 RERLAPRP
tive 82; Mismatches 225;	1 86
QY 99 QYACHDQYAVTILMSPGALGIEFLKGFRVILEEIKSEGRQCQQLILKDPRQLNSSFRRTG 158	Qy 413 LCREGOREWVIG 1:: Db 457 AEQIVPSRMLVI
YFVKV	QY 473 EKLROAKOSSS
Db 339NFTDIELDTDLIPSVIPIESAHDGRC-LCVTENGCSCLAADWKPV 382	Db 516 IRDATHNEP
QY 218 MINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPPKRKTCKQEQTTFTTSCLLQNV 277	Оу 530 ноговреднтк
Db 383 KLTRIEKPPATSNQTEESDGKAEKDKKEDTWT415	Db 571 H
OY 278 SPGDYIIELVDDINTTRKVMH-YALKPVHSPWAGPIRAVAITVPLVVISARATLFTVM 334 Db 416	OY 581 FHPPPLRYREP 1: Db 620 LHLKROSP
QY 335 CRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHANVVQCFAYF 394	Oy 641 LDQDGEARPALI
Db 446 NNKKRASNIHILINENPAFS-HSGSIPL-ILKQSISVLIVY-SHDSAQHEAAVLAFAEL 500	: Db 658 -DED:
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Db 592 INPKYVFFPINKLLQYSIPNSLMTWTTALTEQPARPEQLAGFNQVFARLQAAI 644	C; Accession: T09081
QY 561 CNMHQFIDEEDDWFEKQFVPFHPPPLRTR589	R;Sanchez-Alonso, P.; Genetics 148, 1043-10
DD 645 SRKLNTIESDPOWFENTHHRVATRRVSELEAHNIVPL-PPSLEVKVEDEDAFGQMETLPI 703	A; litte: Olyanization A; Reference number: Z; A:Accession: T09081
QY 590 EPVLEKF	A,Status: preliminary A,Molecule type: DNA

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216557; MUID:98198830; PMID:9539423
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1ty 21:18; Pred; No. 0.091;
Servative 64; Mismatches 149; Indels 94; Gaps 19;
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                                                                                                                                    /2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3 rhabditis elegans hypothetical protein F56D1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: U39997; PIDN: AAA81100.1; CESP: F56D1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L Data Library, November 1995
equence of C. elegans cosmid F56D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F56D1.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y; translated from GB/EMBL/DDBJ
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42;

A: Residues: 1-757 <san> A: Cross references: EMBL: AF030885; NID: 92642221; PID: 92642222 A: Experimental source: strain FB2 C: Genetics: C: Genetics: C: A: A:</san>		cal Similarity: 18.3%; Pred. No. 0.76; 167; Conservative 130; Mismatches 296; Indels 320; Ga NGSQLAVAAQGSGARGADICGWRM-KAAARPRLCVANEGV
C.Keywords: DNA binding Query Match Sec. 2.9%; Score.117; DB 2; Length.757; Best Local Similarity 20.4%; Pred. No. 0.57; Matches J11;, Conseivative 1.56; Mamatches 187; Indels 190; Gaps 27;	tive star on a	GYSNG-DILIMSIPSKGECSPESSANICKLNIGTKSEKIPIASLKWYY 14NSGLYNITEKYDNCTTYLNPVGKHYIADAQNITISQYACHDQ 10
268 ETTSCILONVSPGDYIJELVDDTNTTRKVNHYALKPVBSPWAGPIRAVAITVPL 321 7.7 ETTILILETVALRANGLAKLDYNNIRTHVWOP-GSGRAAPIVLVSTEAAITLAFKE 131 322		OY 106 VAVILMSPGALGIEFLKGERVILEELKSEGROCOQLILGDPROLNSSFRRTGHESOP 163 DD 206 DELEVLGKSGRVYAYDDYNIEKYLIGSGSKSSPSLPRETVVKLPFSDSSSITVGKFLTNP 265 OY 164PLANKFETDYFVKVVPPPSIKNESNTHPFFFRTRACDLLGPD 206 DD 266 SHILMISDE-DYAOLAKDAYPELPFHTYPKESSKSAHPFGFTKKNYYTGGCGTISVW 324
363 RERLAPRPRVFLCYSSKDGQNHANVVOCF-AFFLQDFCGCEVALDLWEDF 411 :		207 NLACKPEWKPR-WINISQHGSDMQVSFDHAPHNFGFRFFTLHY 215 DNTCSFPILVLEKEQIDDVSSKGNALTALHTDSNSRLLVSGDHNGWYRLFRFPEPP 226 KLKHEQPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELV 2385 LTBNSFIPPOGSLKKGNHIVOSYKTKITGSTJCLOROSKHAAIGSDOGHSSIVEVI 2385 LTBNSFIPPOGSLKKGNHIVOSYKTKITGSTJCLOROSKHAAIGSDOGHSSIVEVI
VPGILDLSTKY : VIHLLGPDLLTDF HTROGSRRNYFRS		288 445 333
551 KSGRSLYVAICHMGPTDEEPDNFEKOFVPFHPPLRYREPVLEKFDSGLVLNDVACKPG 610 551 KSGRSLYVAICHMGPTDEEPDNFEKOFVPFHPPLRYREPVLEKFDSGLVLNDVACKPG 610 388 RKTCLRGVLSQLLDQRSDW	· · · · · · · · · · · · · · · · · · ·	483 FESCIVOGFERNYLVVAMRDSSVFA-LDSDTGNMIGTNMIRPRRPERVLYMQILD 381 GONHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWVIOKIHESQFIIVVCS
		DD
RESULT 5 104661. hypothetical protein F8D20.70 • Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Aprilogy #sequence_revision 23.Apr-1999 #text_change 24-Nov-1999 C.Accession: PAAAA		571 POMPERQEVPE
Systems 1, 1970, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heljnen, L.; Vos, P.; Mewes submitted to the Protein Sequence Database, July 1998 A;Reference number: 215381 A;Accession: 704661 A;Accession: 704661 A;Molecule type: DNA A;Residues: 1-917 < GEVy A;Cross-references: EMBL:AL031135 A;Cross-references: EMBL:AL031135 C;Genetics:		DD 8U5 GLSKQKNANRFSNFKGKLKQNAAKNEKSVVTNDEKHEEKNGATVDQIKKKYGFTSS 860 QY 642 DQDGEARPALDGSAALQPLLHTVKAGSPSDHPRDSGIYDSSVPSSELSLPLAEGLSTDQT 701
A.Map position: 4 A.Map position: 4 A.Morens: 137, 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 63.Morens: 18020.70 C.Superfamily: Arabidopsis thaliana hypothetical protein F9020.70 Ouery Match 2.9%; Score 117; DB 2; Length 917;		RESULT 6 T00867. hypothetical protein At2945540 [imported] - Arabidopsis thaliana NA Alternate names: hypothetical protein F172.7 C: Species: Arabidopsis thaliana (mouse-ear cress)

dopsis thallana C; Species: Arabidopsis thaliana (mouse-ear cress)

0.0 0.0		Iminary Ype: DNA Type: DNA 1-901 <sto> rences: GB:AP001510; al source: strain C-1 54</sto>	Best Local Similarity 19.0%; Pred. No. 0.82; Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27; Qy 61 ASINSGLTNITEKTDNCTTYLNYGKHYLDAGNITISOT-ACHOOVAVTILMSPGALGI 119 :	QY 170 ETDYEV	QY 329 TLFTVMCRKKQQENIYSHLDEBSSESSTYTAALPRERLRPPRVFLCYSSKDGQNHMNVV 388 Db 525 KRATVDRRSKEPKNTNQHKNRENRIKRESRFVVL 558 QY 389 QCPAYFLQDFCGCEVALDLWEDFSLCREGQREWYIQKIHESQFILVVCSKGMK 441 : : : : : : 559 RCFWDSPFFIKSDGKQTASFALFOKLARREGGENHIEVIDLSKTYRNRQVVKGIN 612 QY 442 YFVDKKNYKHKGGGRGGGELFLVAVSAIAEKLRQAKQSSSAALSK 488
s. D. J. S. D. S.	A; MCSIGNES: 1-2946 <ssvo-a; 1-1246="" 1.="" 105;="" 1165="" 1210="" 1245="" 1283="" 1309="" 1336="" 1438="" 1638="" 164;="" 1782.7;="" 18="" 1;="" 2="" 2449="" 2481="" 2643="" 2890="" 2931="" 2946;="" 294;="" 2;="" 3="" 314;="" 3;="" 4.="" 40;<="" 652="" 7%;="" 913="" <ssvo-a;="" a;="" at2g45540="" bss="" c;="" cecretics:="" conservative="" gaps="" gene:="" genetics:="" gspdb:gn00139="" indels="" introns:="" l="" length="" local="" map="" matches="" mcsignes:="" mismatches="" no.="" position:="" pred:="" similarity="" td=""><td>2 APWIQLCSVFFTVNACLNGSOLAVAAGGSGRARGADTCGWRAKAAARPRLCVANEGVGBA </td><td>Db 468 LVVESGSGRGRRSSLHFTHAFRPQCWYFIGLEHSCRQGLLGRAESEIRLYIDGSL 522 OY 159 MESOPELNAKEEIDYFVKVVPFPSIKNESNYHPPFF</td><td>261. CKOEGTTETTS</td><td>DD 730 HPGNNEELCRTGGPEILARILSYLLHSLASLDRKHDGVGEEEL-VAAIVSLCGSGKIN 786 QY .384 HMNVVQCRAYFLQDFCGCEVALDLWEDFSLCREGGREWYIQKIHESOPIIVVCSKGMK 441 </td></ssvo-a;>	2 APWIQLCSVFFTVNACLNGSOLAVAAGGSGRARGADTCGWRAKAAARPRLCVANEGVGBA	Db 468 LVVESGSGRGRRSSLHFTHAFRPQCWYFIGLEHSCRQGLLGRAESEIRLYIDGSL 522 OY 159 MESOPELNAKEEIDYFVKVVPFPSIKNESNYHPPFF	261. CKOEGTTETTS	DD 730 HPGNNEELCRTGGPEILARILSYLLHSLASLDRKHDGVGEEEL-VAAIVSLCGSGKIN 786 QY .384 HMNVVQCRAYFLQDFCGCEVALDLWEDFSLCREGGREWYIQKIHESOPIIVVCSKGMK 441

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QY	(a) (a) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	Superfamily: protein-tyrosine kinase, receptor type eph; fibromectin 534-994/ords. APP; inposphotrans ferase), transmembrane protein; tyrosine-sp 539-647/Region: protein kinase ATP-binding motif 339-647/Region: protein kinase ATP-binding motif 329-647/Region: protein kinase ATP-binding motif 32-988/Domain: SAM homology SAM> 30.968/Domain: SAM homology SAM is matches 301; Indels 250; Ga facthes 158; Conservative 122; Mismatches 301; Indels 250; Ga facthes 158; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 122; Mismatches 301; Indels 250; Ga facthes 168; Conservative 168; Con	26) GACTCATGHEPAAKESQCRPCPPGSTKAKQGEGPCLECPPNSTTTSFAASICTCHNNFTR 74 YDNCTTYLNPVGRHVIADAQNITISQTACHDQVAVTILMS-PGALGIEFLKGFR 74 YDN	Db 430 GVSGKSPLPPRTAAVNITTNQAAPSEVPTLRLHSSSGSSLTLSWAPPERPNG- 481 QY 242 REFYLHYKIKHEGPP-KRKTCKQBQTTETTSCLLQNVSP-GDYIIELVDDTNTTRKVHHY 299 10 482VILDIEHKYFEKSEGIASTVTSQMNSVQLDGLRPDARTVVVVRARTVAGY 531 QY 300 ALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVWCRKKQGENIYS 345 1
	of the deve	SVFTVNACL-NGSQLAVAAGGGGRARGADTCGRBAKAARPRIC52	QY 145 KDPROLNSSFRRTGMESQPFLNMRFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQ 204	09 317 ITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRP 368

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De transaction () 有一个有人的一个概则是是是1966年,但	OY) 405 LDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELF 464) 1	QY 465. LVAVSAIAEKLRQAKQSSSAALSKFIAVTFDTSCEGDVPGILDLS:TKTR513- 	QY 514LADNILPQICSHIARSPHGLQEPGQHTRQGSRRNY-FRSKSGR 554	QY 555. SLIVAIGNHHQFIDEEPDWFERQEVPFHPPPLRYREPVLEKED 597. 1.	QY 598 SGLVLANDVACRPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPA 650 DD 817, SASDVWSYGJYWWEVAST-TGERPYDASNQDVINAVEQDYRLPPP 860	QY 651 LDGSAALQPLIHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLHEGG 696, 1 1 1 1 1 1 1 1 1 1	QY 697 STDQTETSSITESVSSSGLGEEPPALPSKLLSSGSCRADIGCRSYTDEL 747 Db 921, VPDYTYFTYGDWLDAIK MGRYKESFVSAGFASFDLVAQMTAEDL 965	RESULT 10	%, Accession: T17112 %, Status: preliminary %, Status: preliminary 1, Molecule type: mRNA 1, Molecule type: mRNA 1, Residues: 1-488, 489-535 < POU> 6, Treatdues: 1-488, 489-535 < POU> 6, Experimental source: mRNA 1, More: the GDNA sequence contains a -1 frameshift near codon 488 1, Company for the GDNA sequence contains a -1 frameshift near codon 488	V. Venerace: A: Note: DKFZp434P211.1	Query Match 2.7%; Score 110; DB 2; Length 535; Best Local Similarity 23.5%; Pred. No. 1.3; Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps	QY 474 KIRQAKQSS-SAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQ 520 103 :	QY 521 LCSHLHSRDHGLQEPQQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQF 578	QY 579 VPFH-PPPLRYREPVLEKFDSGLVLADVMCKFQPESDFCLKVEAA 622 1	OY 623 VIGARG-PADSOHESOHGGLDQDGEARPALDGSAALQPLIHTWRAGSPSDMPRD 675 11:1 1 1 1 1 1 1 1 1	OY 676 SG-IYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSG 732 D

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R;Tellam, J.T.; McIntosh, S.; James, D.E.
J. Biol. Chem. 270, 5857-5863; 1995
A;Title: Molecular identification of two movel Munc-18 isoforms expressed in non-neur
A;Reference number: I49238; MuID:95197608; PMID:7890715
A;Accession: I49239
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submitted to the EMBL Data Library, November 1998
A.Description: Deletion in the beige gene of the beige rat due to recombination betwee
A.Reference number: 217837
A.Accession: T13960
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Holecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                     C:Species: Mus musculus (house mouse) 4. C:Date: 02-Jul-1996 #text_change 05-Nov-1999 C:Accession: 149239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beige protein homolog - rat.
C.Species: Rattus norvegicus (Norway rat)
C.bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C.Accession: T13360
                                                                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 110; DB 2; Length 592; Best Local Similarity 18.5%; Pred; No. 1.5; r. Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps
                                                                                                                                                                                                                                                                          Cross-references: EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g642028
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 LVVISAFATLFTVMCRKKQQ------ENITSHLDEESSESSTYTAALPRERLRPRPK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 -VALDEWEDFSLC-----REGOREWVIOKIHESOFIIVVC-----SKGMKY----- 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 SRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 NLAEDCHNKFKLNIEKLCKTEQDLALGTDAEGQRVKDSMLVLLPVLL--NKNHDNCDKIR 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 AAVLGATGPADSQHGSLDQDGGEARPALDGSAALQPLLHTVKAGSPSDMPRD-SGIY 679
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                                                                                                                                                                                                                                A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-592 <RES>
           407 AVLLYIFGINGTIEEN------
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RESULT 11
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Contractor of

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A;Description: may be involved in cytomatrix organization at the site of neurotransmi
A;Note: component of the presynaptic cytoskeleton
C;Reywords: colled coil; zinc finger
                                                                                                                             A;Cross_references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810 A;Experimental source: strain 129 SVJ C;Genetics:
                                                                                                                                                                                                                A;Nap position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
                                                                      preliminary; translated from GB/EMBL/DDBJ
                                                                                                                     A; Residues: 1-3942 <DIE>
                                                                      A; Status: preliminary
A; Molecule type: DNA
                                              A; Accession: T42730
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Best Local Simi
Matches 156;
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R; Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, Cell Biol. 142, 499-509, 1998
A; Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A; Reference number: 222149; WUID: 98345363; PMID: 9679147
                                       A.C. Cross references: EMB.:AB020019; NID:d1241953; PID:d1035670; PIDN:BAB34688.1
A:Experimental source: strain DA; spicen
C;Genetics:
A:Genetics:
                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1010 RRGEMSVARNQGIMRISQPEMILKEDVSSSTAPEPGFIKKSADRVSELESQHMLDTSAE 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date::11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1125 ------SLSLENILCELRDHLSQSKVAETELAKPLFDALLRVALGNHSADLDPGDT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1175 VPEKSHPS---ERVLSQPGDFSEEAESGCCSLKLLGEEEGYEADSESNPEDGETQDDGV 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKN----ESNY-----HPF-FFRTRACDLILQPDNIACRFFWRRIAISQEGSDMQ. 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796 SCNGVNHIIELNYLDGIRSHSLRAFETLIVSLGEQQRRAAVPGV---DGLDIQQELSSLS 852
                                                                                                                                                                                                                                                                                                                   696 YQNFIFQE--DRLHNTQIASHICNLIQKGNVIVQW------KLYNYIFNPVLQRGV 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RQCQQLILKDPKQLMSSFKRTGMESQPFLNMKPET-DYFVKVVP-----PP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 ELVHHCQOLSI-----TSAQTHMSSQLKQYLPQBVLQIYLKTLPILLKSRVIRDLFL 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 VSFDHAPHNEGFREFYLHYKLKHEGPFRRKTCKÓBQTTETTSCLLQNVSPGDYIIELVDD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-------GPSLHK----GASTDSPCSLK----FFASLRDF 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 TNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISARATLFTVMCRKKQQENIYSHLDE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSESSIY -- TAALPRERLRPRPKVFLCYSSKDGQNHMNVV----QCFAYFLQDFCGCEV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    921 ESEDTSGIDSTASEPLSHILPRISL-------958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 ALDLWEDFSLCREGGREWY--IOKIHESOFI----IVVCSRGMKYEVDKKNYKHKGGGRG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 SGRGELF ---- LVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILD --- 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 --LSTK-------YRLMDNLPQLCSH---LHSRDHGLQEPGQHTRQG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 SRRNYPRSKSGRSLYVAICNMHQFIDEEP-----DWFEKQFVPFHPPPLRYREP 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 VLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
                                                                                                                                                                                                                                                                                                                                                                            80 YLNPVGKHVIADAQNITISQYACH--DQVAVTILMSPGALEIEFLKGFRVILEELKSEG- 136
                                                                                                                                                                                                                                                                            20 GSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTT 79
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                   Ouery Match 2017 2018; Score 108.5; DB 2; Length 3788; Best Local Similarity 19:44; Pred. No. 31; Colembrative 235; Matches 267; Indels 235;
                            έ,
1232 ELPEAEGFSGSIVPNNLLESLTHG 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647 ARPALDG-SAALQP--LLHTVRAG 667
                  A; Residues: 1-3788 CMOR>
                                                                                                                                                                    th
Similarity
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                                                                                                                                                                              Query Match
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C; Accession: T30851
R; Barbosa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.
submitted to the EMBL Data Library, September 1996
A; Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene. A; Reference number: 220903
A; Accession: T30851
                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross references: EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC53011.1
A; Experimental source: strain C57BL/6J
                                                                                                                                                                                                                                                                                                                                      3590 TOWFOR --- PRDARSDRFRHHGGHTVSSSQKRGPARHSYHDYDEPPEEGLWPHD---BGG 3643
                                                                                                                                                                        3535 DTCPQFCS----SHSNPDVQEHYKDGPRAHAYKREEGYMLDDSHCWVSDSRAYHLGQEE 3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3752 AQPQMQGRQAAPGPQQSQPPSSRQT--+PSGTASRQPQTQQQQQQQQQQGGQPQAPQQA 3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lysosomal trafficking regulator, long splice form - mouse
NyAlternate names: belge protein homolog
C:Species: Mus musculus (house mouse)
C;Date: 72-0ct-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                           ----PVLEKF-----DSGLVLNDVMCKPG 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3644 PGRH------TSAKEHRHSDHGRHSGRHAGEEPGRRAAKPHARDMGRHEARPH 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3692 POASPAPAMOKKGOPGYPSSADYSOSSRAPSAYHHASESKKGSRQAHTGPSALQPKADYQ 3751
                                                                                                      E.SIG DNIAQLCSHIHSRDHGLQRPGGHTRQGSRRNYFRSKSGRSLYVAIC-----NAHQFIDEE 570
                                                                                                                                                                                                                                                                                                                                                                                                        611 PESDFCLKVEAAVLGATGPADSQHESQHG-----GLDQDG------EARP- 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 -----ALDGSAALQPLLHTV 664
                                                                     99; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 KAGSPSDMPRDSGIYDSSVPSSELSLPLARGLSTDQTETSSLTESVSSSSGLGEBEPPAL 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GSQLAVAAGGSGRARGADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 19.5%; Pred. No. 40;
%5; Conservative 104; Mismatches 288; Indels 254;
DB 2; Length 3942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 3788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3788 GBAR>
Query Match 2.7%; Score 107.5; 1
Best Local Similarity 19.1%; Pred. No. 39;
Matches 58; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 107; Di
19.5%; Pred. No. 40;
                                                                                                                                                                                                                                                                       571 PDWFERQFVPFHPPPLRYRE-----
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A,Map position: 1
C,Keywords: alternative splicing
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eferences: GB:AE005172; NID:98778345; PIDN:AAF79353.1; GSPDB:GN00141

4	-	Status: preliminary	Ä
	Luros, J.S.; Malti, R.; Marziali, Southwick, A.M.; Sun, H.; Tallon, Davis, R.W. Plant Arabidopsis.	"."A.; Li, J.H.; Li, I.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali Mizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, Rer, M.; Wu, D.; Tu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A.Reference number: A86141; MUID:21016719; PMID:11130712	A A A B A B C
,	., S.; White, O.; Alonso, Creasy, T.H.; Dewar, K.;	ker, J.R.; Palm, C. M.K.; Conn, L.; Cc , B.; Bulzar, L. , 2000	S C S S
	31-War-2001	protein F1504.27 [imported] - Arabidopsis thaliana 5;Species: Arabidopsis thaliana (mouse-ear cress) 5;Date: 02-Mar-2001 fsequence_revision 02-Mar-2001 ftext_change 31-Mar-2001 5;Accession: D66477	7000
		RESULT 15 D86477	58
100 CIRE : 20:1700 BECS	:	1260	: <u>음</u>
Search completed: May 19,	GEI 1259	1209 GEEGGTEADSESNPEDVDTQDDGVELN-PEABGFS-GSIVSNNLLENLTH-	8
Db 617 IFCSL 621	SGLGE- 718	663	ò
DD 571 VFRNNSN QY 559 AICHM 563	COLUMN 662	609 -PGPESDFCLKVEAAVIGA-TGPADSQHESQHGGLDQDGEARPALDGSAALQPLLH	දී දි
DD 554 VFMKPGQY 502 VPGILDLSTKYRLADN	**************************************	DO99 LESLIDICLESARACQORMELELPSQGLSVENILCELREHLSQSKVAETE	2 5
442		1049 RKSADSVRGFQSQF	g
Qy 382 QNEMNYVQCFAYFLQD Db 517NTYWCEV	APDLGFL 1048 JYAICN 562	1012 GGEMSRNENGELIRISYPELTLKGDVSSATAPDIGFL 512 YRLADNLPQLCSHLHSRDHGLQEPGQHTRGGSRRNYFRSKSGRSLYVAICN	g &
		460 KGELFLVAVSAIAEKLROAKOSSSAALSKFI	ð i
Db 417 GESTICSWKGCQDF Qy 327 FATLFTVHCRKKQQEN	GGRGSG 459	4.06 DLWEDFSLCREGOREWYIQKIHESQFIIVVCSKGKKYFVDKKNYKHKGGGRGSG	å . g
OY 267 TETTSCLLQNVSPGDY	AA 960	917	g
OY ZII KPFWKPRNLNISQHG- : 365 HQFTHCKKCNTSLHEV	GCEVAL 405	350 ESSESSIYTAALPRERLRPRPRVFLCTSSKDGC	6
323		290 THITRKVHEYALEPHERWAGPIRAVITYPLVVISARTIL	8 8
Db 275 DIN GOYSCHLODCFY QY 154 FKRTGMESQPFLNMKF	(IELVDD 289	230 VSFDHAPHNPGFRFFYLHYKLKHEGPFKRKTCKGEGTTFTSCLLGNVSPGDYIELVDD **********************************	ଟି ପି
Matches 94; Conservat Qy 94 NITISQIACHDOVAVI	PELPSIA 229	1843 SINKESNY	8 6
Query Match Best Local Similarity	TRDLFL 795	744	ਰ
C;Genetics: A;Gene: F1504.27 A;Map'position: 1			8 8
A; Molecule type: DNA A; Residues: 1-638 <sto> A; Cross-references: GB: AE0</sto>	ELKSEG- 136	80 YANPOKRYIADAQNITISÖYACH - DQVAVTILMSBGALGIEF 10 10 10 1 10 1 10 10 10 10 10 10 10 10	8 6
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                                                     Indels 153; Gaps
                                                                                                  NITISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCOQLILKDPKQLNSS 153
                                                                                                                                                                                                        FKRTGMESQPFLNMKFETDYFVKVVPFP---SIKNESNYHPFFFRTRACDLLLQPDNLAC 210
                                                                                                                                                                                                                                          KPFWKPRNIAISQHG--SDMQVSFDHAPHNFGFRFFTLHTKLKHEGP--FKRKTCKQEQT 266
                                                                                                                                                                                                                                                                                                                                            GESTIC--SNKGCODFVLDV-----RCISVLEYFIHKSHEH-------PIFISTS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NITWCEV------CERQLDPREWFITCNK-----CCITIH-------LECIFGS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRN--YFRSKSGRSLY-V 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-----FRNNSHTRQLCTMCHNCTGL----IFTEGIRRHATYINHSNRSTHRM 616
                                                                                                                                    FATLETVMCRKKODENIYSHLDEESSE-SSTYTAA-LPRE---RLRPRPKVFLCYSSKDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNEMNIVVOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWYLQKIHESOFIIVVCSKGMK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGD 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEM------SIERDIYGKVQ 570
Atch 2.7%; Score 106.5; DB 2; Length 638; ocal Similarity 19.4%; Pred. No. 3.1; 94; Conservative 63; Mismatches 175; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mpleted: May 19, 2003, 09:25:43
: 38:7988 secs
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us-09-912-157-2.rsp

GenCore version 5.1.4_p5_4578 Copyright (c) 1993_c 2003_c compugen Ltd.
ON protein - protein search, using sw model
Run on; J. C. C. May 19, 2003, 09:08:53. p. Search time 15:2893. Seconds (without alignments)
Title:
Scoring table; BLOSUM62 Gapert 0.5 Gapert 0.5
Searched: 112892 segs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB Seq length: 0 Minimum DB Seq Length: 2000000000000000000000000000000000000

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries Database : SwissProt_40:*

	, , 				SUMMARIES	Ş	2
Result No.	Score	.Query Match	Length	DB	. ·		Description
-	310	1.7	998	ļ	117R HUMAN		O96f46 homo ganten
.;	306	7.6	864	4	117R MOUSE		mus
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~	110	2.7	592	٦.	STB3_MOUSE		EUM.
∞	104	7.6	1462	÷	PTP6_DROME		P16620 drosophila
6	103.5	9 .6	663	-	RGP2_HUMAN		P47736 homo saplen
01	102	5.5	828	Ä	ABR HUMAN		omou 6
1	101	2	1275	-	GNRP_HUMAN		Q13972 homo sapten
17	100.5	2.5	974	ન_	RHG6_HUMAN	٠,	S homo
E1	99.2	2.5	794		Z151_MOUSE		l mus m
7	66	2.5	783	٠.	ZFY2_MOUSE		2 mus
12	66	2.5	970	-	PSU1_YEAST		0 sacc
16	98.5	2.5	993	-	EPB3_MOUSE		-
17	98.5	2.5	1050	-	EX5B_CHLPN		
87	86	7.7	820	÷	CTNB_TRIGR		P35223 tripneustes
19	97.5	2.4	1845	-	Z236_HUMAN		_
50	26	7.7	984	-	EPB1_CHICK	•	gallu
21	- 1	7	984	-	EPB1_RAT		rattus
27	96.5	7.4	746	۲.		•	P00521 abelson mur
73	96.5	7.7	902		EPBB_XENLA		091736 xenopus lae
24	96	7.	424	-1	- 1		_
	96	7	. 660	-	HT31_ARATH		-
56	96	2.4	1114	-	E2K3_MOUSE		09z2b5 mus musculu
27	95	7.	.828	-	CAN_DROME		Q11002 drosophila
78	95	7.7	.933	-	PRGR_HUMAN		
53	56	7.	1036	-	AXO1_CHICK		ੱ
30	94.5	7.7	351	٦	HM14_CAEEL		P20271 caenorhabdi
31	94.5	2.4	770	-	GIT1_RAT		
35	24.5	7	841	⊣.	IE63_MCMVS		154 murine
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Euteleostomi; /Murinae; Mus. ainter S.L.,		rotein. N-17 REC! LAR (POTENT) C (POTENT) GLCNAC.	SEQUENCE 864 AA; 97807 MM; 343FD51AA687DA31 CRC64; Query Match 7.64; Score 306; DB 1; Length 864; Best Local Similarity 22.54; Pred: No. 1.16-15; Matches 189; Conservative 128; Mismatches 319+ Fedels203; Ga 40 GWRM	OY 87 HVIADAQNITIGGRADGNAVT-ILMS-PGALGIEERKGERVILEELKSERGROOG	QY 231 SPDHAPHNEGERETIHKILREGPFKRKTCKQEQTTETTSCLL 274
FT CARBOHTD 225 225 N-LINKED (GLCNAC.) (POTENTIAL) FT CARBOHTD 242 N-LINKED (GLCNAC.) (POTENTIAL) FT CARBOHTD 265 265 N-LINKED (GLCNAC.) (POTENTIAL) FT CONFLICT 367 367 V -> N-(IN REF. 1) FT CONFLICT 580 580 H -> R-(IN REF. 1) FO SEQUENCE 866 AA, 96131 MM-203308ED2303BDC9 CRC64; QUERY MATCH QUERY MATCH Best Local Similarity 23.1%; Pred-100, 5.4e-16; Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;	09 . 69 NITEKIDING, TITLIAPUGKHVIADAQNIT. Db . 49 NCTVKISTCLDDSWILEP	Db 216 QLRVSFTLWRESTHTQILLTSFPHENENSCFEHUH-HIPAPRPEEFHQRSNVTLTLRNLK. 274 OY 371 SCLLQNVSEGNTIELVDDTNYTRKYHHYALKPYHSPHACPIRAVAITVPLVVISAF 327 Db 275 GCCRHQVQIQPFFSSCLNDCLRHSATVSCPENPDTPEPIPDTMPLMYPTTGISILLVG 334 OY 328 ATLETVMCKKQOENIYSHLDESSESSTYTAALPREHLRPRPKVFLCTSSSGGON 383 :::	CYRLADNLPQL RYPLADRFEEV SEPDWFE IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db CHRAPLYRE FG CH CH CH CH CH CH CH C	RESULT 2 ILTR_MOUSE ID ILTR_MOUSE ID ILTR_MOUSE AC 660943 AC 16-JUN-2002 (Rel. 41, Created) DT 15-JUN-2002 (Rel. 41, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) BT 15-JUN-2002 (Rel. 41, Last annotation update) GN ILLTR.

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Uliggs; AACS2357.1;

WGI:107399; Ili7.

L 31 POTENTIAL.

L 32 864 INTERLEURIN-17 RECEPTOR.

NR 32 824 INTERLEURIN-17 RECEPTOR.

NR 32 824 INTERLEURIN-17 RECEPTOR.

NR 32 824 INTERLEURIN-17 RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAQNITISQYACHDQYAVT-ILWS-PGALGIEFLKGFRVILEELKSEGRQCQQ--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LELQPDNIACKPFWKPRNINI----SQH------CSDMQV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---NLSVSSTQHGELVPVI.HVEWTI.QTDASILYLEGAELSVI.QLNTNERL.CVKRQF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------HAPHNEGENFFYLHYKLKHE---GPFKRKTCKQEQTTETTSCLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKQIFAPRQEEFHQRANVTFTLSKFHWCCHHYQVQPF-FSSCLND-----CLR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGDYIIELVDDTHTTRKVMHYALKPV--HSP-WA-GPIRAVALTVPLVVISAFATL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPCPVI----SNTT-----VPKPVADYIPLMVYGLITLIAI----LLVGSVIVL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRKKQOENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 306; DB-1; Length 864; similarity 22.5%; Pred: No. 1.1e-15; Conservative 128; Mismatches 319+ Endels-*2037 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------KAAARPRL-----CVANEGVGPASRNSGLYNITPRYDNCTTYLNPVGK 86
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CITOPLASMIC (POTENTIAL).
POLY-GLU.
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97807 MM;
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3422
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3432
344
314
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308
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342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPR-KVWIVYSA-DHPLYVEVYLK 399
                                                                                                                                          391 FATFLODFCGCEVALDLMEDFSLCREGOREWIOK -- - IHESOFIIVVCSKGMKYFVDK .446
                                                                                                                                                                                          447 KNYKHKGG-------GRGSGKGELFLVAVSALAEKLRQAKQSSSAALSKFLAVYFDY 496
                                                                                                                                                                                                                                                                                                                             :| | :: | | :: | | 455_AKWRAILGWABPAVQLRCDHWRPADLETAAMMHLLPDFKR---;-PACFGTIVVCTFSG;509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 RSLYVAICHMHÖFIDEEPDWFEKQFYPFHP---;PPDRR--:TREPVLEKFDSGLYLMDVM 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 ROLKEAVLREGEWOTQCPDWFERENICLADGODLPSLDREGVFEDPLLPP-GGGIVKOOPL 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKPGPESDFCLKVEAAVLGATGPADSGHESGRGGLDQD------GEAR 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 VRELP-SDGCLVVDVCV-----SEEESRNAKLDPQLWPQRELVAHTLQSMVLPAEQV 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649 PALDGSAALQPILHTVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL---- 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 PA---AHVVEPLHLPDGSGAAAQLPMTEDSEACPLLGVORNSILCLPVDSDDLPLCSTPM 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN

JIS_HUMAN

STANDARD, PRT, 502 AA.

105-UNAN GRAL4; QORRA5;

115-UNA-2002 (Rel. 41, Last sequence update)

15-UNA-2002 (Rel. 41, Last annotation update)

15-UNA-2003 (Rel. 41, Last annotation update)

15-UNAN-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----MEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSTDE 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 MSPDHLQGDAREQLESIALSVLQQSLSGQPLESWPR-PEVVLE------GCTPSEE 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDILINE-20273223; PubMed-10815801;
Tian E., Savyer J. N., Largaespada D.A., Jenkins N.A., Copeland N.G.,
Shaughnessy J.D. Jr.;
"Evi27 encodes a novel membrane protein with homology to the IL17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20317118; PubMed-10749887;
Shi Y., Ullich S.J., Zhang J., Connolly R., Grzegorzewski R.J.,
Shi Y., Ullich S.J., Zhang J., Connolly R., Grzegorzewski R.J.,
Barber N.C., Mang W., Wathen R.; Bodge V., Fisher C.L., Olsen H.,
Ruben S.M., Knyazev I., Cho Y.H., Rao V., Wilkinson K.A.,
Carrell J.A., Ebner R.;
A novel cytokine receptor-ligand pair. Identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization, and in vivo immunomodulatory activity. ...
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
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NCBI_TaxID-9606;
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Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117S_HUMAN
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                                                                                  Goddard A.D., Yangucka M., "Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yangucka M.L., Wood W.I., Gurney A.L.; Goddard A.D., Yangucka M.D., Yandlen R.L., Wood W.I., Gurney A.L.; Til-17Rhl., "IL-17Rhl.,"

J. Biol., Chem. 276.1660-1664(2001).

I. FUNCTION: Receptor for the proinfilammatory cytokines IL17B and IL17B: May play a role in controlling the growth and/or differentiation of hematopoietic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> VKFSELLMGGKGHRRLFHHSLLLRMSSLLSNALLPADT
                                                                                                                                                                                                                                                                                                                                                                 mostly
                                                                                                                                                                                                                                                                                           Secreted (isoform 2).

- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here), and 2; are sproduced by alternative splicing.
-- TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly in fetal and adult liver; kidney, pancreas, testis, colon, brain and small intestine; notidetected in peripheral blood leukocytes, lymphoid organs, and most cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 RASYVIPVTGDSEGATYQLIPYPPTCGSDCIRHKGTVVLC---PQTGVPFPLDNNKSKPG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 NANMANEDGPSMSVNFTSPGCLDH------IMKYK------KKCVKAGSLMDPN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 -----KQEQTTE---TTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AVAITVPLVVISAFATL------FTVMCRKKQQENIYSHLDEESSESS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 NLNISOHGSDMQVSF-----DHAPHNFGFRFFYLHYKLKHEGPFKRKTC----- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPYFPICGSDCIRHKGTVVLCPQTGVPFPLDNNKSKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing SIGNAL 1 \ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ITACKKNEETVEVNETTTPL----GNRYMALIQHSTI-----IGFSQVFEPHQKKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 113;
                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Type I membrane protein (1soform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN REF. 1).
L -> I (IN REF. 1).
LIPPLA -> SSPCI (IN REF. 2).
MISSING (IN REF. 2).
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 3.4%; Score 135.5; DB 1;
Best Local Similarity 20.1%; Pred. No. 0.0078;
Matches 76; Conservative 49; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF208110; AAF86051.1; -.
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468
502 AA;
                                                                     PubMed-11058597;"
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                                               FUNCTION.
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OV 387 VVOCRAYELODECGCEVALDIAREDESICREGOREMVIOKIHESORTIVVOSKOMRYFVUR 446	<u> </u>	Oy, 641 LDODGEARPALDGSAALQPLLHTVK
3.7 TICEPREPIONIC SERVIT ENGINEER AND ACTUAL AND ACTUAL CONTINUED OF SERVICE AND ACTUAL ACTUA		Db 658 -DEDDVDLQPHASH
	·	Qy 699 DQTETSSLTESVSSSGLGEEEPPA
447 KNIKHKGGGRGSGKGELFLVAVSAIABKIRQAKQSSSAALSKFIAVIFDYSCEGDVPGIL		DD 691 SESDSSSESESESDNEGEDPKT
SPSENSO-DLFPLAFNLFCSDLRSQIH		
RLMDNLPQLCSHL 525	<u>~</u>	RESULT 5
Db 461 SVCPKTHIAKDATAFCAEL 479	M H	EPB3_HUMAN STANDARD; ID EPB3_HUMAN STANDARD;
		P54753;
RESULT. 4 The second se		Dr. Ul:OCT-1996 (Rel. 34, Created) Dr. 01-OCT-1996 (Rel. 34, Last sec
TSO2_CAREL TO VEOL CHAMBARD.		
010128;		DE kinase receptor 3 precu DE kinase receptor HEK-2).
DT		GN EPHB3 ON ETK2 ON HEK2.
01-FEB-1996 (Rel.		Eukaryota;
DS Hypothetical 81.6 kDa protein F56D1:2 in chromosome II precursor. GN F56D1.2.	-	OC Mammalla; Eutherla; Primates; OX NCBI Parit-9606;
Caenorhabditis elega		
OC EUKATYOTA; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; OC Rhabditidae; Peloderinae; Caenorhabditis.		
NCBI_TaxID-6239;	. 62	MEDLINE-93390963; PubMed-8397
	OK D	RA Boehme B., Holtrich U., Wolf G RA Strobhardt K Buchgamen-Walcm
STRAIN-Brist		RT. *PCR mediated detection of a n
	2 0	2.";
	<u> </u>	L Oucogene 8:283/-2884(1993). C -1- FUNCTION: RECEPTOR FOR MEM
This SWISS-E	_	C EPHRIN-B1 AND -B2.
		C: -1: CATALITIC ACTIVITY: ATP + C: tvrosine phosphate.
use by non-profit institutions as long as its content is in no	·	C -1- SUBCELLULAR LOCATION: Type
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or send an email to license	-	C -1- SIMILARITY: CONTAINS 2 FIB
AAA8		C -1- SIMILARITY: BELONGS TO THE C. RECEPTOR SUBFAMILY.
WormPep; F56D1.2; CE01		
SIGNAL 1		C Inia SWISS-PROF entry is copyr C between the Swiss Institute o
CHAIN		European Bloinfor
SEQUENCE 718 AA; 81	J.O	C modified and this statement is
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Best Local Similarity 21.1%; Pred. No. 0.064; Matches 82; Conservative 64; Mismatches 149; Indels 94; Gans 19;	-	CC
The state of the s		
		DR Genew; HGNC:3394; EPHB3. DR MIM: 601839; -
Db 398 RDKVRSREVRNIALIEFVKVMIVYAD-DNDLHTDCVKKLVENLRNCASCDPVFDLEKLIT 456		InterPro; IPR001090; InterPro: IPR000719:
QY 413 LCREGGREWVIGKIHESGFIIVVCSKGMKYFVDKRNYKHRGGGRGGRGELFLVAVSAIA 472.		InterPro; IPR003961;
DD 457 ABQIVPSRWLVDQISSLKKFIIVVSDCAEKILDTEASETBQLVQARPFADLFGPAMENI- 515		IPR0019862; IPR001660;
QY 473 EKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRD 529		DR InterPro; IPR001245; Tyr_pkina DR InterPro; IPR001426; YRase_rec
DD 516IRDATHNFPRARKKYAVVRFNYSPHVPPNIAILALDT-FILDEGFAGLTAFLENVE 570		Pfam; PF00041; fn3; 2 Pfam; PF00069; pkinas
Qy 530 HGLOBPGQHTRQGSRRNYPRSKSGRSLYVAICNNHOPIDEEPDWFEKOFVP 580		N Pfam; PF00536; SAM; 1. N Pfam; PF01404; EPH lbd; 1.
57] :: :: :: :: S7] H		rs; PR00014;
211 H TOWARD TOW		R Probom: PD000001; Euk pkinase;

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yright. It is produced through a collaboration of Bloinformatics and the EMBL outstation. Institute. There are no restrictions on its tions as long as its content is in no way is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).
OVICKPGPESDFCLKVEAAVLGATGPADSQHESQRGG. 640:
                          | | : : | : : |
| ED---RIAASIKYNLVPPQALVDSD---657
                                                                            KAGSPSDM -- PRDSGIYDSSVPSSELSLPLAMGCLST -698
                                                                                                                 SHONOPLILIPPEOCG-----BDSD----SD 690
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UITOUS.
MA DOWAIN TYPE III-LIKE DOWAINS.
HE TYR PAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7371;
G., Luzlus H., Grzeschik K.-H.,
gmann H.;
new human receptor-tyrosine-kinase, HEK
                                                                                                                                                                                                                                                                                                                                    d).
equence update)
nnotation update)
cursor (EC 2.7:1:112) (Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBERS OF THE EPHRIN-B FAMILY. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + a protein tyrosine - ADP + protein
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CTIVVK 716
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eceptorV.
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514 -- LLOWING OLCH HIRS ROBGIO BEGORT -- -- -- ROGS RRNT - PRSKSGR 554
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                                                                                                                              SSS SLYVI-AIC-----PLANGELDERPOWERGFYPHPP-----PLAYREP----VLEKFD 597
                                                                                                                                                                                                                598-S-----GLVLMDVMCKPQPRSDFCLKVBAAVLGAFGPADSQHESQHGGLDQDGEARPA 650
                                                                                                                                                                                                                                           817. SASDVWSYGIVWWENWS-------TGERPYWDMSNDDVINAVBQDYRLPPP 860
                                                                                                                                                                                                                                                                                                                       651 LDGSAALOPILLHTVKAGSPSDMPRDSGIYDS-----SVPSSELSLPLMEGL 696
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                               s. (),
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DR Probom; PD001495; Ep.

DR SHART; SH00464; SAM: 1.

DR SHART; SH00464; SAM: 1.

DR SHART; SH00464; SAM: 1.

DR PROSITE; PS00107; PROTEIN_KINASE_DAF; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_DAF; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TRR 1.

DR PROSITE; PS00109; RECEPTOR_TRKIN_V.1; 1.

DR PROSITE; PS00109; SAM_DOMAIN; 1.

DR PROSITE; PS00105; SAM_DOMAIN; 1.

DR PROSITE; PS00105; SAM_DOMAIN; 1.

TRAINSÉCIASE; TYTOSINE-POTCEIN KINASE; ATP-binding; Phosphorylation; KW Trainsferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; KW TRAINSÉCIASE; TRAINSMANDAN, 1.

STORAL 3. 998 EPHRINI TYPE-B KECEPTOR 3.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 19.0%; Pred. No. 0.78;
Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 GADTCGWRMKAAARPRLC-----VANEGVGPA-----SRNSG-----LYNITFK 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 A--LKPVH----SPWAGPIRAVAITVPLVVISAFATL-----FTVMCRKKQDENIYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ-BINDING MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 N-LINKED (GLCNAC. . .) (POI 110286 MW; 5708203970061103 CRC64;
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MISCELLANEOUS: EVI27 is a common site of retroviral integration in BXHZ murhoe myeloid leukemias, localized near the ILLTBR gene.
Proviral integrations result in increased expression of ILLTBR on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted (isoform 2).
ALTERNATURE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
TISSUE SPECIFICITY: LIVER and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myelold
IITS_MOUSE STANDARD; PRT; 499 AA.

G9JIP3; 09JIP2;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1355292; Ill7br.
Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1.AND 2).
MEDIJINE-20273223; PubMed-10813801;
Tian E., Saware J.R.; Largaespada D.A., Jenkins N.A., Copeland N.G. Shaughnessy J.D. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor: 1,2098-2109(2000).

-1. FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differenciation of hematopoietic cells.

-1. SUBCELLUIAR LOCATION: Type I membrane protein (1soform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encodes a novel membrane protein with homology to the IL17
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INTERLEUKIN-17B RECEPTOR.
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us-09-912-157-2.rsp

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205 SKLAQLVEKKLEDYYKIDEKGLIKGKTQSQLLIIDRGFDPVSTVLHEL------ 252
                                                                                                                                                                                                                                                                                                                                                                                                 488 KFIAVYFD-----YSCEG-DVPGIL----DLSTKYR-----LADNLPOLCSHLH 526
                                                                                                                                             321 LVVISAFATLFTVMCRKKQQ-----ENIYSHLDEESSESSTYTAALPRERLRPRPK 371
                                                                                                                                                                                                                                  87 SYDCFLADFGSKSEKKYKAAYIYFTDFCPDSLFNKIKASCSKSIRRCKEINISFIPQESQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                             253 TFQAMAYDLIPIENDTYKYKTDGKEKEAVLEEDDDLWVRVRHRHIAVVLEEIPKLAKEIS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 -VALDLWEDPSLC-----REGOREWICKIHESOFILVVC-----SKGNKY------ 442
                                                                                                                                                                                                                                                                                               147 VYTLDVPDARYKTSPDPSNASRKEVVMEAMARQ--IVTVCATLDENPGVRYKSKPLDNA 204
                                                                                                                                                                                                                                                                                                                                   443 -----FYDKK----NIK.--HKGGGRGSGKGELFLV-----AVSAIABKLRQAKQSSSAALS 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence.update)
15-JUN-2002 (Rel. 14). Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphoydrolase).
PTF69D OR.DPTP.
Drosophila melanogaster (Fruit fly).
Enkaryota: Macaoa: Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta: Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophila.
                                                                           Query Match 2:7%; Score 110; DB 1; Length 592; Best Local Similarity 18:5%; Pred. No. 0.92; Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps
                                                                                                                                                                    34 IMLLDEFTRILSSCCKNTDLLEEGITVIENIYKNREPVROMKALYF-----ISPTPK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90046860; PubMed-2554325; Streull M., Krueger N.K., Tsal A.Y.M., Salto H.; Ruceger N.K., Tsal A.Y.M., Salto H.; and faceptor-linked protein tyrosine phosphatases in humans and Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein transport.
SEQUENCE V. 592 AA; 67942 WW; 7874B71DE107871A CRC64;
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InterProf IPR001619; Sec1-11ke. Pfam; PF00995; Sec1; 1.
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Best:Local:Similarity (1:20.0%; - Pred. No. 9.4;
                                        88; Conservative
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                       -1 SIMILARITY: CONTAINS 2 PIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE PHOSPHATASE DPTP. EXTRACELLULAR (POTENTIAL).
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FIBROWECTIN TYPE-III 1:
PROTEIN-TYROSINE PHOSPHATASE 1:
PROTEIN-TYROSINE PHOSPHATASE 2:
                                                                                                                                                                                                                                                                                                                                                                                       Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167411 MW; F8091D69E88230EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPIASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                             GLCNAC:
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ROSITE; PS50056, TIR PHOSPHATASE 2; 2.
ROSITE; PS50055, TIR PHOSPHATASE PTP; 2.
Ydrolase; Receptor; Glycoprotein; Signal; Treell adhesion; Immunoglobulin domain; Repeat.
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N-LINKED
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InterPro; IPR003006; Ig_MRC.
InterPro; IPR003509; Ig_C2.
InterPro; IPR003609; Ig_like.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
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Pfam; PF00047; 1g; 2.
Pfam; PF00102; Y_phosphatase; PRINTS; PR00700; PRIYPHPHASE.
                                                                                                                                                                            TyBase; FBgn0014007; Ptp69D.
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SURRT; SN00060; FN3; 3.
SHART; SN00410; IC_11ke; 1.
SMART; SN00409; IC_2; 1.
SMART; SN00409; PPPC; 2.
                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Receptor;
Cell adhesion; Immuno
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1462 AA;
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Length 1462;

DB 1;

2.6%; Score 104;

Query Match

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53; Mismatches 136; Indels 164; Gaps 23;
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-1- SUBCELLOTAR LOCATION: Associated with Golgi membranes.
-1- TISSUE SPECIFICITY: Significant expression seen in the brain, kidney and pancreas. Abundant in the cerebral cortex and expressed at much lower levels in the spinal cord. Not detected in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY, AND INDUCTION.

MEDILINE-98010655; PubMed-9346962;

Kurachi H., Rada Y., Tsukamoto N., Maeda M., Kubota H., Hattori M.,

Iwai K., Minato N.;

"Human SPA-1 product selectively expressed in lymphoid tissues is a
specific GPPase-activating protein for Rapl and Rap2.";

J. Biol. Chem. 273:28081-38088 (1997).

-I- FUNCTION: Gtpase activator for the nuclear ras-related regulatory
protein RAP-11, converting it to the putatively inactive
GDP-Dound state.
                                                                                                                                                                                                                                                                                                                                   -----KQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALK---PVHSPWAGPIR 313
                                                                        232
                                                                                                                                                                                                                                                                                                                                                                                                                               463 DVPKTPNGKVVSYLIHLIGNPMSTVDREMMGPKIRRIDEPHHKTLYESVSPNTNYTVTVS 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AVAITVPLVVISAFATLFTVMCRKKQQE-----NITSHLDEES---SESSTYTAALPR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 -----ONITISOYACHDOV------AVTILWSPGALG-IEFLKGFRVILEEL 132
                                                                                                                                                               319 OPTOYPOGITILSY --- DPIFIPKVETTGSTASTITIGWNPPPDLIDYIOYYELIVSE- 374
                                                                                                                                                                                                                    133 KSEGRQCQQLILKDPRQLNSSFRRTGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPF 192
                                                                                                                                                                                                                                                                                                                                                                                 375 -- SG------EVPKVIEEAIYQQNSRNLPYM-------FDKLKTATDIE-- 408
                                           55 NEGVGPASR -----NSGLYNITFKYD------NCTTYLNPVGKHVIADA 92
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MEDLINE-91256304; PubMed-1904317;
MEDLINE-91256304; PubMed-1904317;
MEDLINE-91256304; McCormicar S., Clark R., Conroy L., Watt K.,
Crosler W.J., McCormick F., Polakis P.;
"Molecular cioning of a GTPase activating protein specific for the
Krev-1 protein plural.";
Cell 65:1033-1042(1991).
                                                                                                                                                                                                                                                                                                        193. FFRTRACDLLLQPDNLACKPFW.: -----KPRNLNISQH-----GSDMQVSF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
Rapl GTPase activating protein 1 (RaplGAP).
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ew; ; 60(erPr	GTP		666	15-JUN-1999. 15-JUN-2002: Active break
E PE	Interprof IRVOUGSID: RAP, GAP. Fig. Program Program Program Program Program Program Program Colors I.	· · ·	888	
GTPASE & COMAIN SEQUENCE	ictivation; dembrane. 210 397 RAP/RAN-GAP. 5 663 AA; 73391 MW: 3703B7Cc60340bA CRC64:	<u>.</u>	8888	Mammala; Eutheria; Frimates; C NCBI_TaxID=9606; [1] SEOTENCE PROM N.A.
Query Match Best Local	2.6%; Score 103.5; DB 1; Length 663; Similarity 19.5%; Pred. 190.3:4; Advantable 25.	<u> </u>	2225	TISSUE-Hippocampus; MEDLINE-94086546; PubMed-8262969 Tan EC.: Leung T., Manser E.,
, E	ESNYHPFFFRTRACDLLLO		222	Ine numen active breakpoint clus brain protein with homology to gu and GTPase-activating proteins.;
1	EEDIIPYPSVHEVLGREGPFPLILLPOFGGTWIEGTNHEITSIPETE		RRE	
707	07VIACKPFWKPRNINISQHGSDMQVSDDARPHNFGFREFIZHK 249 71 PLQSPTIKVKLECNPTARIYRKHFLGKEHFNTYSLOTALGHLVFSLKYD 119		2 2 2	TISSUE-Fibroblast; MEDLINE-93352461; PubMed-8349582; Beisterkamp N., Kaartinen V., var
250 L	250 LKHEGPFKRICKGEGITETISCLLQNVSPGDIIIELVDDTNTIRKVHHYALKPVH 305 :		R R R R	"Human ABR encodes a protein wit. DBL nucleotide exchange factor dJ. Biol. Chem. 268:16903-16906(1
306 SPV 174. YPI	306 SPHAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIISHLDEESSESSTYTAALP 362		5 X X X	SEQUENCE OF 436-597 FROM N.A. MEDLINE-8006/847; PubMed-2567217; Helaterkamp N., Moria C., Groffe "ABR, an active RCR-related gene."
363 REF 226		<u> </u>	¥888	70 50 50
	QREWVIORIHESQFIIVVCSKGMKYFVDKKNYK : :	4 11 1 1	38888	NATIVE PRODUCTS: FORM; ARE PRODU
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	GDVPGILDLSTKYRLADNILPQLCSHLASRD-HGLQEPGQHTRQGSRRNYF-	<u></u>	8888	This SMISS-PROT entry is copyrig
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		•	3888	EMBL; U01147; AAC50063.1; EMBL; 119704; AAC37519.1; FROT: 110705; AAC37519.1;
648 RPI 536	RPALDGSAALQPILHTVKAGSPSDMPRDSGIYDSSYPSSELSLPLMEGLSTDQTE 702 :	. •	5888	Genew: HGNC:81; ABR. MIM; 600365; InterPro; IPR00008; C2.
,		-	DR	InterPro; IPR001331;

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HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER
LIGHG AND MUSCLE...
S I DBL-HOMOLOGY (DH) DOMAIN.
S I PH DOMAIN.
S I RHO'GAP DOMAIN.
TO HUMAN BCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3349582;
V., van Soest S., Bokoch G.M., Groffen J.;
In with GAPrac activity and homology to the actor domain.*;
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PATING PROTEIN FOR RAC AND CDC42. PROMOTES :
CDC42-BOUND GDP BY GWP, -WHERENFY-ACTIVATING
1262969;

br E., Lim L.;
Int cluster region-related gene encodes a lint cluster of granine nucleotide exchange proteins eins.;
27298(1993).
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annotation update)
region-related protein.
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2587217;
, Groffen J.;
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16-0CT-2001 (Rel. 40, Created).
16-0CT-2001 (Rel. 40, Last sequence update)
15-0KT-2002 (Rel. 41, Last annotation update)
Glandine nucleotide releasing protein (GNRP) (Ras-specific nucleotide exchange factor CDC25).
RASGREI OR CDC25.
                                                                                                                                                                     STANDARD; PRT; 1275 AA.
                                                                                      1. A. S. J. J. A. V. .
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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013972;
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Best Local :
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2.5%; Score 102; DB 1; Length 859;
Best Local Similarity 20.5%; Pred. No. 6.4;
Matches 117; Conservative 57; Mismatches 190; Indels 208; Gaps
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R InterPro: IPR001849 PH.

R InterPro: IPR001891 RhoGAP

R InterPro: IPR001891 RhoGAP

InterPro: IPR001891 RhoGAP

R Ffam: Pr00169 PH: 11

R SWART: SW00323 PH: 11

R SWART: SW00324 RhoGAP; 1.

R PROSITE: PS50004; C2_DOMAIN 2; 1.

R PROSITE: PS50004; PH_2; 1.

R PROSITE: PS50009; PH_DOMAIN; 1.

PROMAIN: 301 459 PH

PDOMAIN
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                                                                                                                      SEQUENCE FROM N.A.

PROJECTOR OF A PURPORT OF A PURPORT OF A PARK W., Brook D., Well W., Das B., Park W., Brook D., "Cloning and analysis of human cDRNs encoding a:140-kDa brain guanine nucleotide-exchange factor, Cdc25GEF, which regulates the function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 2.5%; Score 101; DB 1; Length 1275;
1 Similarity 19.2%; Pred. No. 13;
98; Conservative 66; Mismatches 144; Indels 202;
                                                                                                                                                                                                                                                                                                     Gene 151:279-284(1994).
--- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
--- SIMILARITY: CONTAINS 2 PH DOMAINS.
--- SIMILARITY: CONTAINS 1 DBL-EUNOLOGY (DH) DOMAIN.
--- SIMILARITY: CONTAINS 1 RAS-GEE. DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSJOULLY,
PROSITE; PSOU741; DH_1; 1.
PROSITE; PSO0720; GDS_CDC25; 1.
PROSITE; PSO50095; 10; 1.
PROSITE; PS500095; PH_DOWAIN; 2.
Guanine-nucleotide releasing factor; Repeat.
                                                                                                          t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
InterPro; IPR000219; RhoGEF.
Pfam; PF00169; PH; 2.
Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L26584; AAA58417.1; -. Genew, BGNC; 19875; MASGREI. LINTEPPO; IPRO01331; GDS_CDC24. IINTEPPC; IPRO00048; IQ_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00013; PH; 2.
SMART; SM00147; RASGEF; 1.
SMART; SM00129; RASGEF; 1.
SMART; SM00125; RhoGEF; 1.
PROSITE; PS00010; DH_2; 1.
PROSITE; PS00710; DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00617; RasgeF; 1.
Pfam; PF00618; RasgeFN; 1
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038 1275 AA;
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8 6	126 RVILEBLKSEGRQCQQL-ILKD-5-3-PKQLNSSFKRTGME-345SQPFLANKPETDYFYK 176 : :	
. & A	177 VVPPPSIKNESNYHPFPPRTRACDLILQPDNIACKFWKRPKINISQ=====BGSDMQVS 231:	
ă	FDHAPHNFGFRFFILHYLKHEGPPKRKTCKOBOTTETTSCLLQNVSPGDYIIELVD	
8 8	347 LAHCKONRDFDKLLKHYRAKPD	
. 8	HYPHEHVERNSLDYAKSKLEELSR	
ργ.	HIDERSESSITTAALPREKLRERPKVFLCTSSKOGGNADNVVOCFATFLODFCGCEVAL	
g . ;	TILLE COLLEGE	
3 8	- -	
. <u>A</u> .	441 KXEVDKKNYKARGGG-FILLELVA 467	
g	507 GGKLHLTKNGVISLIDCTLLEEPRSTBEEAKGSGQDIDHLDFKIGVEPRDSPPFTVLVA 566	
<u>સ</u>	468 VSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHS 527	
δ	557	
8	609RRTREGTREGEN-SRSDASLE. 628 (20) v v v v v v v v v v v v v v v v v v	
RESILA	2 F11	
RHG6	HUKAN	
328	KEGO HUMAN STANDARD; PKT; 9/4 AA. 043182; 043437; Q9P183; Q9UK81; Q9UK82;	
555		
58	(Rel. 41, ctivating	
N N	() () () () () () () () () () () () () (
88	8 (Human)	
888	Mammalla; Butherla; Primates; Catarrhin; Hominidae; Homo. NCBI_TaxID-9606;	
≅£	[1] SEQUENCE FROM N.A., REVISIONS, FUNCTION, SUBCELLULAR LOCATION, AND	
₽ £	IVE SPLICING.	
25	1286; PubMed-106991 Paylor R., Jenna	
2 2 2 5	. Mancini M.A., Zoghbi H.Y.; tilonal analysis of ARHGAP6, a novel GTPase-activ	
2 12 2	Minoh.; Hum. Mol. Genet. 9:477-488(2000).	
5 2 2	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). MEDLINE-98086484: Pubhed-9417914:	
2 2 2	i H.Y.; a novel rho-type GTPase-activati	
E E		
코 8 1	Genomics 46:268-277(1997). -1- FUNCTION: GTPASE ACTIVATOR FOR THE RHO-TYPE GTPASES BY CONVERTING	
ខ្លួន	STATE. SULES WOR CYT	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PASHETP (IN ISOPORM 2) | PASHETP (IN ISOPORM 2) | FASHETP (IN ISOPORM 1) | FASHETP (IN ISOPORM 2) | FASHETP (IN ISOPORM
                                                                                                                                                                    RHO-GAP.
MISSING (IN ISOFORM 4 AND ISOFORM 5).

E -> ELELTDIGILGTRPPMNSDTHRNFDPTATLRNG
(IN ISOFORM 2).
SPDMLQSEVSFSVGGRHSSTDS -> TSSVLPAAVQACPQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.5%; Score 100.5; DB 1; Length 974;
Best Local Similarity 18.6%; Pred. No. 9.9;
Matches 178; Conservative 99; Mismatches 294; Indels 385; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 -----SGLYNITFKYDNCTTYLNPVG-----KHVIADAQNITISQYACHDQVAVTILWS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 PGALGIEFLKGFRVILEELKSEGROCOOLILKDPROLNSSFRRTGMESOPFLNMKFETDY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 GGPNGI------SRGHPYVVWKSEGDF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VKVVPFPSIKNESNYH----PFFFRTRACDLLLQ----PDNLACKPFWK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 TWNSMSGRSVRLRSVPIQSLSELERARLQEVPFYQLQQDCDLSCQITIPKDGQKRK---K 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 PRNLNISQHGSDMQVSFDHAPHNFGFRFFYL----HYKLKHE------G 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 AGGSGRARGADICGWRMKA------AARPRICVANEGVGPASRN-------64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPase activation; SH3-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                1. SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZMBL; AF117067; AAF43261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF17765; AAD53166.1;
AAT17765; AAD55087.1;
AF01272; AAC98539.2;
AF022212; AAC98540.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR000198; RhoGAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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CONFLICT
SEQUENCE
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VARSPLIC.
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762 Service RAGECSISQG-NISPAWPRWQGSP-FF------AELDS----------7792
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                                                                  290 THTTRKVMH-------TALKPVHSPWAGPIRAVAITVPLVVISARAIL- 330

    36, Last sequence update)
    40, Last annotation update)
    16 (Polyomatius late initiator promoter binding (Zinc finger protein 213)

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-1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT
                             317, PPGNKRONKELSSSNSSLSSTSTPN -- ESTSPNTPEPAPRARRGAMSVDSITDLDDN 373
                                                                                                         1374 GSRLLEALQLSLPAEAQSKKEKARDKKLSLNPIYR------OVPRLVDSCCQHLE 422
                                                                                                                                      331 FINAL PROPERTY SHIPS - --- BSSESSTYTAAL PREPARENCE 374
                                                                                                                                                                   423 KHGLQTVQIPRVGSSKRRVRQLREEPDRGIDVSLERERSVHDVAALLKRELRDMPDPLLT 482
                                                                                                                                                                                                               375 7-CYSS. -----KDGOHHMAVVQCBARLQDECGCEVALDIWB-------DPSLCREG 417
                                                                                                                                                                                                                                              418 Q---------REWIQ---KIHESQFIIVVCSKGMKYEVDK 446
                                                                                                                                                                                                                                                                                                                                                                                                       596 ENTE------ALEMVPPDLQNEVLISLLETDPDVVDYLLRRRASQSSSPDMLQSE 644
                                                                                                                                                                                                                                                                                                                                                                                                                                        487 -----VPGILD 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .542 QEVTGHKMTSLNLATIFGPHLLHKQKSSDKEFSVQSSARAEESTAIIAVVQKMI----- 595
                                                                                                                                                                                                                                                                                                                                                                          .447 KNYKHKGGGRGSGKGELFLVAVSALAEKL-------RQAKQSSSAAL---- 486
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MEDLINE-96003919; PubMed-7575457;
Schulz T.C., Ropwood B., Rathjen P.D., Wells J.R.E.;
"An unusual arrangement of 13 zlnc fingers in the vertebrate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 DMPRD----SGIYDSSVPSSELSLPLAMEGLSTDQTETSSLTESVSSSSGLGEERPP 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rapp L., Carmichael G.G.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
---- OTTETTSCLLQNVSPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZISI_MOUSE STANDARD; PRF; 79.06081; 66608.
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence upd
16-JUC-2001 (Rel. 40, Last annotation u
Linc finger protein 151 (Polyomavirus 1
protein) (LP-1) (Zinc finger protein z
ZNF151 OR ZFP100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 SGRGELFLVAVSALAEKLRQAKQSSS-----AALSKFIAVTFDYSCEGDVPGILDLST 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ACHTLKSLAEPSSTIGESADASAVEGGDKRAKDEKAAATMLSRLGQARGSSSTGPGRELK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Mismatches 146; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 CGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK-YFVDKKNYKHKGGGRG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 KIRLMDNLPQLCSHL-HSRDHGLQEPGQH------TRQGSRRNYFRSKSGRSLY 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 VAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLVLANDVMCKPGPESDFCL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------VELKPDPTSSMA- 206
             -1- SUBCELLULAR LOCATION: Niclear (Potential).
-1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRIONIC AND ADULT TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 CDCTFVVD-GVDF------KAHKA--VLAACSEYFKMLFVDQKDVVHLDISNA 67
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS50097; BTB; 1.
PROSITE: PS00097; BTB; 1.
PROSITE: PS50157; ZINC_FINGER_C2H2.2; 13.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                          -1- SIMILARITY: BELONGS TO THE KRUEPPEL PAMILY OF C2H2-TYPE SINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 99.5; DB 1; Length 794;
20.6%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86664 MW; FFF88E56EDEBF7ED CRC64;
REGULATES THE EXPRESSION OF SPECIFIC GENES!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 EERGGQAESASSGAEQTEKADAPREPPP------
                                                                        FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2H2-TYPE
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                                                                                                                                                                                                                                       U14556; AAA85493.1; -...
P08046; 1A1H.
                                                                                                                                                                                                                                                                                        MGD; MGI:107410; Zfp100.
InterPro; IPR000110; BTB_POZ.
InterPro; IPR000822; Znf_C2H2.
Pfam; PP00095; zf-C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 20.6% Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muclear protein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00225; BTB;
SMART; SM00355; ZNF_C;
PROSITE; PS50097; BTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297.
297.
3325.
409
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618 KVEĄAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSG 677

the received Act

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Matches 117; Conservative O.74; Mismatches 1207; Indels 1210; Gaps 34;
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207 AARARALSESSEQUENEVERARGE-EDGQEEEGGAGFATVKEEGHE-IDNGEPPEERESA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein.
2 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
7 ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLUTAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS. 2FX/ZFY. SUBFAMILY.
                                                                                                                                                                                                                                                      Mus musculus (Mouse):
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus
NCBL_Faxib-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
ROSITE; PS50157; ZINC_FINGER_C2H2_2; 10.
TRASCTIPTIOn_regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                   NEDLINE-89168416; PubMed-2493989;
Mardon G., Page D.C.;
The sex-determining region of the mouse I chromosome encodes
protein with a highly acidic domain and 13 zinc fingers.";
Cell 56:765-770(1989).
                                                                                                                                                        . T. 1 Tests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 99; DB 1; Length 783; 19.2%; Pred. No. 9.6;
                                               678 IYDSSVPSSELSLP---LMEGLSTDQTETSSLTESVSSSGLGEE 719
                                                                         1722D1C23F019DF8 CRC64;
                                                                                                                                                     PRT; 783 AA. ...
                                                                                                                                                                                                                                                                                                                                                                                                           1- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR
                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Last sequence update)
16-02-2001 (Rel. 40, Last annotation update)
2. Zinc finger Y-chromosomal protein 2.9
EFF2.OR.EFF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MCI:99213; EF92.
InterPro; IPR000822; Enf. C2H2.
Ffam; PP00096; 2: C2H2; 13.
PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                  (Rel::17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M24401; AAA56845.1; -.
PIR; A31491; A31491.
HSSP; P08048; 52NF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88856 MW;
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00355; ZnF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754
783 AA;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding;
                                                                                                                                                                                  01-FEB-1991
01-FEB-1991
                                                                                                                                                      ZFY2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZN_FING
SEQUENCE
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211
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71. TEKYDNCTITLNPVGKHVIADAQNITISQTACHDQVAVTILMSPGALGIEFLKGFRVILE 130
                                                                                                                                                                                                               375. KSKKKRPESKQYQSAIFVAPDGQT÷÷----LRVYPCHFCGKKFKTKRFLK÷-++RHIK : 423
                                                                                                                                                                                                                                                                                     185: NESNYHPFFFRTRACDILIZOPDNIACKPFWKPRNILNISQHGSDMQVSFDHAPHNFGFRFF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449°-LHNHWESH----KLINTEKTTECDDC-RKNLSHA-----GTLCTHKTMHTE---- 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 ------RGVNKTCKCKFRODYETARQTILINHILLVVHRKK-----FPHICGECGKGFRH 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 TAALPRE-RLRPRPKVFI.C---1SSKDGQN---HMNVVQCFAYFLQDFCGCEVALDLWE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 DFSLCREGGREWVI---OKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLV 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 HTKAYPHKCDMCSKGFHRPSELKKHVATHKSKKWHQCRHCDFNSPDPFLLSHHILSAHTK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 TRLMONLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEP 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 SGFKRHVISIHTKDYPHR-----GFRRPSE 768
                                                                                                                                                                                                                                                                                                                                                                                                                              245 YLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 HSPWAGPIRAVAITVPLVVI---SAFATLFT----VMCRKKQQENIYSHLDEESSESSTY 357
                                                                  339 TAATDNNSDEL SECTION EVONATASAMLHHDESG ---- GLD ---- RVPKQ 374
                                                                                                                                        131 ELKS----EGROCOQUILKDPRQLMSSFKRTGMESQP--FLANKFETDYFVKVVPFPSIK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-97245296; PubMed-9090055;
MEDLINE-97245296; PubMed-9090055;
de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from chromosome XIV of
Saccharomyces cerevistae reveals an unusually high number of
overlapping open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 AVSAIAEKLRQAKOS--SSAALSKFIAVYFDYS-----CEGDVPG-----ILDLSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 DWFEKOFVPFHPPPLRYREPVLEKFDSGLYLNDVMCKPGPESDFCLKVEAAVLGATGPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota/Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                    reagoloff A.A.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
mRNA decapping protein 2 (PSUI protein)
DCP2 OR PSUI-OR YML118C OR N1917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 - SQHESQH 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769 KNQHIMRH 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-4932;
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PSU1_YEAST
ID PSU1_YEAST
AC P53550;
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Local Similarity

Best

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                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial
(See http://www.18b-81b.ch/announce/
                                                                         -1- FUNCTION: REQUIRED FOR THE PRODUCTION OF ACTIVE DECAPPING ENZYME, PERHAPS IN A PROCESS REQUIRING THE HIDDRISTS OR A PYROPHOSPHATE BOND. DECAPPING IS A THE MAJOR PARHWAY OF WANA DEGRADATION IN YEAST. IT OCCURS THROUGH DEADENYLATION, DECAPPING AND SUBSEQUENT 5' TO 3' EXOMOCLEDLITIC DECAY OF THE TRANSCRIPT BODY.
-1- SUBJUNIT: INTERACTS WITH DEPL.
-1- SIMILARITY: BELONGS TO THE NUDIX HYDROLAMS PAMILY. STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 LONVSPGDYIIE--LV------DDINTTRKVMHYALKPVHSPW--AGPIRAVALTVP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLKIKSFAQLIIKLCPLVWKWDI--RVDEALQQFSKYKKSIPVRGAAIFNENLSKILLVQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GTESDSWSFPRGKI----SKD----ENDIDCCIREVKE----BIGFDLTD----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 2.5%; Score 99; DB 1; Length 970;
Best Local Similarity 17.9%; Pred. No. 13;
Matches 106; Conservative 86; Mismatches 182; Indels 218; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LENVISVORILEDILVRFIINCPNEDLSSVERELFHFE----EASWEYTDFIKLMNPTLP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 LVVISAFATLFTVMCRKKQOENIYSHLDEESSESSTYTAALP------RERLR----- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQ 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REWVIQKIHESQFIIVVCSKGNKYFVDKKNYKHKGGGRGSGKGELFLVA-VSAI----- 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YIDDNQFI------ERNIQGKNYK------IFLISGVSEVFNFKPQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 ----AEKLR--QAKQSSSAALSKFIAVYFDYS------CEGD 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 VRNEIDKIEWFDFKKISKTMYKSNIKYYLINSMWRPLSMWLRHORQIKNEDQLKSYAEEQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DHGLQEPGQHTR 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---MHQFIDEEPDWFE----KQFVPF- 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- HPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFC 616
Dunckley T., Parker R.; The DCP2 protein is required for mRNA decapping in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 P -> L (IN REF. 1).
108667 MW; D53CA2C5A546FA4A CRC64;
                                            cerevisiae and contains a functional Nutr motif.";
EMBO J. 18:5411-5422(1999),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPGILDLSTKYRLMDNLPQLCSHLHSR------
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                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (sor send an email to licensefisb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S0005062; DCP2.
Pro; IPR000086; NUDIX_hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ram; PF00293; NUDIX; 1.
RINTS; PR00502; NUDIXFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               L43065; AAA68866.1; -
                                                                                                                                                                                                                  POMBE SPAC19A8.12
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436 4
425 4
970 AA;
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CONFLICT
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MEDLINE-21824237; PubMed-11802165;
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
Sef is a feedback-Induced antagonist of Ras/MAPK-mediated FGF signaling.";
Nat. Cell Biol. 4:170-174(2002).
EMBL: AF424804; AAL79530.1;
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01-JUN-2002 (TrEMBLrel: 21, Last amnotation update)
$Imiliar expression to FGF protein (Fragment).
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84.6%; Pred. No. 5.6e-231;
ive 34; Mismatches 49;
PKVFLCTSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDF
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(TrEMBLrel, 21, Last anno
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Matches 496; Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygili, Neopterygil, Teleostel, Ostariophysi, Cypriniformes,
Cyprinidae, Banio.
NCBL_TaxiD-7955,
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Tsang M., Friesel R., Kudoh T., Dawid I.;
Tidentification of Sef. a novel modulator of FGF signalling.";
Nat. Cell Biol. 4165-165(2002).
EMBL, A2364103; AAL76112.1; -:
SEQUENCE 745 AA, 83431 MW; 56FEIF0B9D98DDB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.9%; Score 1961; DB 13; Length 745;
llarity 51.4%; Pred. No. 1.1e-170;
Conservative 114; Mismatches 197; Indels 58
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Q8QEL9;
01-JUN-2002 (TFEMBLEEL, 23
01-JUN-2002 (TFEMBLEEL, 23
01-JUN-2002 (TFEMBLEEL; 23
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Watches 390; Conserva
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119 -IEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESOPFLNMKFETDYFVKVV 178
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MEDLINE-99069613; Pubmed-9851916;
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Y64G10A.6.
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299 YALKPUBSPRÄGPIRAVÄITYPLVVISARATLETVNCRKKQOBNIYSHLDEESSESSTYT 358
                                                                                         344 TALSADRPWPRPIFICISSEDGARHIAVIQSPAFFLQDPCGCEVSLDLWEHLEICKEGQ 403
                                                                                                                                                                                                                                                                                                        419 REWVIQKIHESQFIIVVCSKGMKTFVDKKNYKHKGGGR-------GSGKGELFLVA 467
                                                                                                                                                                                                                                                                                                                                                404 MSWLSRRIDBAHFIITVGSKGLKHFYERRHREKRATSKERNREPSASDSSSSSRDLETVA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                           527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDHÖLORPÖGHTROGSRRNYFRSKSGRSLXVALCNMHQFIDBEPDWFEKQFVPFHPPPLR 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             588 YREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVL-----GATGPADSQHESQHGG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 LDQDGBARPALDGSAALQPLLHTVKAGSPSDNPRDSGIYDSSVPSSELSLPLANGGLSTDQ 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 SSQD------AGSCRPVLHTDGSASPPEMPRDSGIYDSSVPSSELSIPLADGLSPDH 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ASRNSGL--YNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVTILWSPGALG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEMDEGARKLGVTERYDNCSVNWSPLGKHAIHEVNNISFSHLSCDSQAAVVVHWAASPLG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (zebrafish) (zebra danio).
Eukaryota: Motazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Stafinopterygili, Neopterygil; Teleostei; Ostariophysi; Cypiniformes; Cypinidae; Danio.
NCBI_FaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAHFFMASCLFLCYTASVNG------GKRGNSDKCSYK-------QGTQT 43
                                                                                                                                                                359 AALPREKLRPRPKYFLCTSSKDCQNHANWWQCFAYFLQDFCGCEWALDLWEDFSLCREGQ
                                                                                                                                                                                                                                                                                                                                                                                                                              468 VSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNIPQLCSHLHS
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Ras/MAPK-mediated FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ:databases.
EMBL; AF401232; AAL78897.1; - SEQUENCE 745 AA; 83437 MW; 75BB9EDCC08A4652.CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 ADMSSLADSVSSSSGLGDERPPAVSSLHCTAHTICKADL 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OJ-UNN-2002 (TrEMBLrel. 21, Created) (01-UNN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 TETSSLTESVSSSSGLGEEPPALPSKLLSSGS-CKADL 738
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Furthauer M., Lin W., Ang S.L., Thisse B.
"Sef is a feedback-induced antagonist of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t. Cell Biol. 4:170-174(2002).
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468 VSAIAEKLRQAKQSSSAALSKFIAVTFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHS 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDHGLQEPGGHTRQGSRRNYFRSKSGRSLYVAICNNHQFIDEEDDWFERQFVPFHPPPLR 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 PPPWFINDSFPPPSFIRTNSCEVILGPDNIVCRPFWRPKMIAVSQLGSNIHVVFDHAPST 223
                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                                                                                           REWVIOKIHESOFIIVVCSKGMKYFYDKKNYKHKGGGR------GSGKGELFLVA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
179. PPPSIKNESNYHPPFFRTRACDLLLQPDNIACKPFWKPRNLNISQHGSDMQVSFDHAPHN
                                                                                                                        FGFRFFTLHTKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDF11ELVDDTNTTRKVMH
                                                                                                                                                    359 AALPRERLRPRPKVFLCYSSKDGQNEIMVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%; Score.170.5; DB 5; Length 846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ainscough R.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Science 282:2012-2016(1998).
EMBL; ALI10498; CAB54470.1; -
SEQUENCE 846 AA; 94852 MW; 613AEF55EBB89EA4 CRC64;
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01-007-2000 (TrEMBLRel. 15, Last sequence update)
01-DEC-2001 (TrEMBLRel. 19, Last annotation update)
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Best'Local Similarity 18.1%; Pred. No. 0.098;
Matches 133; Conservative 105; Mismatches 239; Indels 257; Gaps
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                                                                                                                                                                                                              53 VANEGVOPASRNSGLYNITEKIDNCTT-----ILMPVGKHVIADAQNITISQIACHDQV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 CKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVP 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371. KVFLCYSSKDGQNHMNVVQCFAYFLQDF-CGCEVALDLWEDFSLCRBGQREWVIQ---KI 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 HESQFIIVV------CSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLR 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 RGGTMETDDHMGGIPARNSKGERLLLYI------GIIDILQSYRFVKKLEHSW 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 SHL-HSRDH-GLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNWHQFIDEEPDWFEKQFVP 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        581 FHPPPLRYREPVLEKFDSGLVLNDVNCKPGPESDFCLKVEAAVEGATOPADSGHESQHGG 640
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                                                                                                                                                                                                                                                                                                                                                        107 AVTILWSPGALGIEFLK-GFRVILEELKSEGROCOQLILKDPRQLNSSFKRTGMESOPFL 165
                                                                                                                                                                                                                                                                                                                                                                                                                107 DVIMODFTVVESIFFPSEGSNLTPAHHINDFREKTYA------143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 -----TFKD-----LDFLQDIPDGLFLDADMIN--ALCKTLQRDCLVLQSFKI 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166: NMKFETDYFVKVVPFPS----IKNESNYHPFFFRTRACDLLLQPDNIACKPFWKPRNINI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420, KALVHDGDTVSVHRPGFYAERFOR------FMCN-----TWCN----TVFKK--IP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 LKPSPSK-----KPRSG---SSFSRRAGSSGNSCITYQPSVSG-----EHKAQ--- 494
                                                                                                                                                                                                                                                                                 1 MASASSGPSS - SVGFSSFDPAVPSCTLSSAASGIKRPMASEVLEARQDSYISLV----- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 VQHKEAE-----PLOKLLPGYYM-------PP
                                                               7.1 62.9%; Score 117:55; DB 4%; Length 562; Y 18.1%; Pred. No. 0.098;
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Eukaryota; Fugi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
SEQUENCE 1.562 AA; 62633 MW; A8F7988EB73506A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998.(TrEMBLrel. 05, Last sequence update).
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Telomere-associated recQ-like helicase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757 AA.
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Query Match 2.9%; Score 117; DB 10; Length 917; Best Local Similarity 18.3%; Pred. No. 0.23; Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps ~42; Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Ξ. 92 NGSRVSV----GYSNG-DILIMSIPSKGECSPESSAMICKLNLGYKSEKIPIASLKWYY 145 --GPASR------NSGLYNITFKYDNCTTYLNPVGKHV---IADAQNI--TISQYACHDQ 105 --FLANKEEIDY-----FVKVVPFPSIKNESN---YHPPF-----FRTRACDLLLQPD 206 NLACK----PFWKPR-NLNISQHG-----SDMQVSFDHAPHNFGFRFFYLHY 248 385 ITENSFIPEQGSIKKONNHIVQSVKIKLFGSITCIQKSQNSKHLAIGSDQGHDSLVEVI 444 288 DDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFT------- 332 333 ------VMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRFKVFLCYSSKD 380 381 GQNHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCS--- 437 ------KGMKYFVDKKNYKHKG------GGRGSGKGELFLVAVSAIAE-----K 474 572 IYIYSLAHVVQGVKKVLHKKKFSSSPICSASTFYGTSGVG---LTLVFTDGTVEIRSLPE 628 19 NGSQLAVAAGGSGRARGADTCGWRM--KAAARPR----LCVANEGV-----58 LSQLKQTSIRGFTYSSPKPNSLPEITISASWDGDLVMVNGDDELIVSSVLPQKETFRLVE 688 Koetter'P., Rempel S., Entlan K.-D., Hohelsel J., Jesse T., Heljnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. D------ALTPVY-------LQVSLVDIEEANVLYTKHIASDICPGIISLQ 483 PESCIVQGFEKNYLVVAMRDSSVFA-LDSDTGNMIGINMIKPK-----KPFKVLYMQILD 106 VAVTILMSPGALGI -- EFLKGFRVILEELKSEGROCOOLILKDPKQLNSSFKRTGNESQP 206 DELEVICKSGRVIAYDDIMIEKYLIQSQSKSSPSLPRETVVKLPPSDSSSITVGKFLTNP 325 DATCSFPILVLELKROIDQDVSSRQNAALTALHYDSNSRILLYSQDHWUNLYRERPPY 249 KLKH-----EGPFKR-----KTCKQEQTTETTSCLLQNVSP------GDYIIELV LRQAKQS-----SSAALSKFIAVIFDYSCEGD------VPGILDLSTKYRLMD EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
1- SIMILATITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AL031135; CAA20026.1;
EMBL; AL031135; CAA20026.1;
EMBL; AL061897; CAR80272.1;
InterPro; TRR001689; WM40. Hypothetical protein; Repeat; WD repeat. SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;

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669 SMNXYENDVSVCHEGIIISSSPREKKSMEGSVEKTRSREGETTOTEDESSERIERI. 744		Db 393 ATWIYIRSF
571 DORFERO POPE	3	
HANVENSREINTITKVEDEEELDIDDIDIDDDHHPNQQQGERPKEQGILS	х Д	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
599 GLVLNDVMCKPGPESDFCLKVEAVLGATGPADSQHESQHGGL	о <u>п</u>	OY 122 LKGFRVILEI
642 DODGEARPALDGSAALQPLLHTVRAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQT 701 : : : : : : :		OY 159 MESOPFLAM
DEMGAAKHANIJKK	Д	523 Y
702 ETSSITESVSSS 714	à	. 503
BOST EMECTAKSESSTA YOL	<u></u>	554
RESULT 9	ò —	261
4 OG4634 PRELIMINARY; PRT; 2946 AA.		b 613 -KARESSIL
1) -1000 (myphotyc) 07 (montod)	ð	301
(TrEMBLrel. 07, Last	Δ	b 670 MKPVESFWA
oz (TremBirel. protein.		Qy 335
Aric45540. Arabidopsis thaliana (Mouse-ear cress).		Db 730 HPGNNEELC
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;	-	Ov 384 HMNVOCEA
eurosids II; Brassleales; Brassleaceae; Arabidopsis.		787
TO TO THE PARTY OF		
SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;		Oy 44.2
20083487; PubMed-10617197; Kaul S. Rounsley S.D. Shea T.P.		DD 837 OLLLDGCRR
T., Mason T.M., Bowman C.L., Barnstead M.E., Feld	ð	y 486 -LSKFIAVY
K., Kerchum K.A., Lee J.J., Konning C.M., Koo .A., Shen M., Vanaken S.E., Umayam L., Tallon		DD 897 DLRRLLGFI
	· ·	OY 539 TROGSRRNY
S.L., Fraser C. e and analysis o		: Db : 957 AKTGEDNVL
Chaliana."; Nature 402:761-768(1999).		QY 599 GLVLNDV-M
2.1 BOURNCE FROM .N.A.		DD 996 NPHDNEIGE
STRAIN-CV. COLUMBIA; Lin X.:		OV 657 LOPLINEYE
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.		-
EMBL; AC003680; AAC06163.1;		
interfro; IPROUD4U9; Beige_BEACH. InterPro; IPRO01680; WD40.		Oy 717 GEEEP
Pfam; PF02138; Beach; 1.		DD 1075 NNVYNVDNS
MJ FEOUROUI WD40; 3. MD0n; PD000018; WD40; 1.		
ProDom; PD007848; Beige_BEACH; 1. SMART; SM00320; WD40; 3.		RESULT 10 09KE04
PROSITE; PS50197; BEACH; 1.		ID Q9KE04 PR
REPGAL; MD IEPEAL. SEQUENCE 2946 AA; 321930 MW; B162CFBDEB5D3372 CRC64;		T. 01-JUN-2002 (
Query Match 2.9%; Score 117; DB 10; Length 2946; Bost Form Similarity 18 7%: Dred No. 1 4.		N BH1054.
rative 105; Mismatch		C Bacteria; Firm
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ANTELOPECCEVALDLARDFSLCREGREWIGKIHESOPITVVCSKGMK--441
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                                                                       TRAGSPSDMPRDSGITDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGL 716
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillacee; Bacillus.
WCBL_TaxID-86665;
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[TrEMBLrel. 15, Last sequence update)
[TrEMBLrel. 21, Last annotation update)
[08]/ABC transporter (ATP-binding protein).
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188 ------NETSLILEWSEPRDIGGRDDLLYNVICKKCRGSSGAGGPATCSRCDDNVE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 SLVIAPRACIANAVEVSVPLKLYCNGDGEWMVPVGACTCATGHEPAAKESQCRACPPGSY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 KAKOGEGPCLPCPPNSRTTSPAASICTCHNNFTRADSDSADSACTTRRSP-PRGVISNV- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 NITISOTACHDOVAVTILWS-PGALGIEFLKGFRVILEELK-SEG-----RQCQQLIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 KDPKQLNSSFKRTGMESQPFLNMKPETDYFVKVVЎFPSIKNESNYHPFFFRTRACDLLLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 FVPROLGLIERRVHIS-----HLLAHTRYTFEVQAVNGVSGKSPLPPRYAAVNITTNQAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 PDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGPRFFYLHYKLKHEGPF-KRKTCKQ 263
                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BI SIMILARITY).
-1- SIMILARITY BELONGS TO THE ITR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 SVFFTVNACL-NGSQLAVA----AGGSGR---ARGADICGWRMXAAARPRLC----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 VANEGVGPA-----SRNSG------LYNITFKYDN------CTTYLNPVGKHVIADAQ 93
                                                                                                                                                   Query Match (1987) 2.9%; Score:115.5; DB 11; Length 938; Best Local Similarity 19.4%; Pred. No. 0.33; Matches 160; Conservative 120; Mismatches: 285; Indels 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN.KINASE_TRY; 1.
PROSITE; PS00790; RECEPTOR_TR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TR_KIN_V_2; 1.
GROSITE; PS00791; RECEPTOR_TR_KIN_V_2; 1.
Glycoptotein; Kinase; Phosphorylation; Receptor; Repeat; Transmembrane; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 938 AA; 103997 MW; 8D128CA46F19E73F CRC64;
01-NOV-1996 (TrEMBLYS) 01, Last sequence update)
01-JUN-2002 (TrEMBLYS) 11, Last annotation update)
Protein Kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD: MGI:104770; Ephb3.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR001090; Euk_pkinase.
InterPro; IPR003962; Full_repeat.
InterPro; IPR003961; Full_repeat.
InterPro; IPR001560; SAM.
InterPro; IPR001245; TY_pkinase.
InterPro; IPR001456; Kase_receptorV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom: rouvodol; Euk pkinase; 1.
SWART; SMO0060; FNR: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U11493; AAA67925.1; -.
HSSP; P29323; 184F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0014; ENTYPRIT:
PRINTS; PR00109; TYRKINASE;
ProDom; PD000001; Euk pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00060; FN3; 2.
SMART; SM00454; SAM; 1.
SMART; SM00219; TYPKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1
                                                                                                                                                                                                                                            NCBI_TaxID-10090;
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             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
2.9%; Score 116.5; DB 16; Length 901;
Best Local Similarity 19.6%; Pred. No. 0.25;
Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GLEE-----RQN 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ASRNSGLYNITFKIDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILWSPGALGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 NINISQHG-----SDMQVSFDHAPHNFGFRFFTLHTKIKHEGPFKRKTCKQEQTTET 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 KRATVDRASKEPRINGHKINEN-----STREE-----STREE-----STREEVINGHKINEN-----STREEVINGHKINEN------STREEVINGHKINEN------STREEVINGHKINGHKINGH STREEVINGH STREET STRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 MFIERGENVGLLGPNGAGKSTTISMISSLIQPTSGDVLIKGGSIHKQSKAIRSILGVVPQ 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 EIDIEV-----KVVPP-PSI-----KNESNYHPFFFRTRÄCDLLLQPDNLACKPFWKPR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 ARDFKVECESCEGCPFRPECTRARGINGVHYINPVY------EELKAKQHQKLK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 ISCLLANVSPGDYIIELVDDINTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIS-AFA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 TLFTVMCRKKQQENIYSHLDEBSSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMRVV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 QCF---AYFLQDFCGCEVALDIMEDFSLCREGOREWV----IQKIHESOFIIVVCSKGMK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 YFVDKKNYKHKGGGRGSGKGELFLVAVSAI------AEKLRQAKQSSSAALSK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 FIAVYFDYSCE-----GDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EFLKGFRVILEELKSEGR ----- QCQQL -- ILKDPKQLNSSFKRTGMESQPFLNMKF 169
                                                                                                                                                                                                    *Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

**INITARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 ----SEEGRILYQKRKIDVESVEGHVKQNIGFRRIHIRGK----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C-125 / JOH 9153;
STRAIN-C-125 / JOH 9153;
MEDLINE-2051258 Publied-11058132;
MEDLINE-2051258 Publied-11058132;
MERLINE B. Nakasone K., Takaki Y., Maeno G., Sasaki R., Mašul 1
Fuji F., Hrama C., Nakamura Y., Ogasawara M., Kuhara S.,
Borikkoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000006; ABC_transportr; 1.
SNART; SN00322; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport; Complete proteome.
SEQUENCE 901 AA; 104585 MW; E519406E650B2CBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             673 EIAVYHDLTARENLAFFGKIYGLKGEELKHR-MESTLOLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 938 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBJ, AP001510; BAB04773.1;
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001559; Transposase_11.
Pfan; PP00005; ABC_tran; 1.
Pfan; PF01609; Transposase_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q60669 PRELIMINARY; PRT;
Q60669;
01-NOV-1996 (TJEMBLTel. 01, Created)
                          SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
Q60669
ID Q60669
AC Q60669
DT 01-NO
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45;

Gaps

	**	. /						
173 YEVKVVPPPSIKNESNYHPPFFRTRACDLLLQPDNLACKPFHRPRNLNISQHGSDM 101: YEVESIFPSEGSNLTPAHHYNDFRFTTA	QY 3.28 ATLEYWACKKQ	QY3 434 VVCSKGMKYEVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQ 477 QY3 51HNIDAQRELESTQYSVORTH	QY 529 DH-GIORPGGERRINIERSKSGRSLTVAICUMHQFIDEEDDWFEKQFVPFHPPPLR 587 11	RPALDGSA VTTKA SSLTESV : :	Db 534 STILEKL 540 RESULT.13 Q94460 ID Q94460 PRELIMINARY; PRT; 348 AA.	AC 094660; DT 01-MAR-2001 (TEEMBLEAL 16, Created) DT 01-MAR-2001 (TEEMBLEAL 16, Last sequence update) DT 01-MIN-2002 (TEEMBLEAL 11, Last annotation update) DF 01-MIN-2002 (TEEMBLEAL 11, Last annotation update) DE BA415A6.2 (Similar to connexin): (Fragment)	Manualia: Eucheria; Primates; Catarrhini; Hominidae; Color Catarrhini; Hominidae; Hominidae; Catarrhini; Hominidae; Homi	DR. PELNTS; PRO0206; CONNEXIN. DR. SEART; SM00037; CONNEXIN. DR. PROSITE; PS00400; CONNEXINS_1; 1. DR. PROSITE; PS00400; CONNEXINS_2; 1. FT. NOW_TER SQ. SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;
<u> </u>	1)	and the second s	enter i victore della	an Cardina				
<u> </u>		and the same of th	enter i ar abe dan	a '				·
			eren eren eren eren eren eren eren eren	an Cardina			<u> </u>	32;
Db 393 PSEVPTLHSHSTSGSSLTLSWAPPERPNGVILDYEMKYFEKSKAIAS 439 Qy 264 EQTTETTSCLLQNVSP-GDITIELVDDTNTRKV	QY 428 ESOFITVVCSKGMKYFVDKKNYKHKGGGRGGKGELFLVWYSAIAEKLROAKOSSS 483 DD 590	534 EPGQHT		SUL 975				Ouery Match Best Local Similarity 18.1%; Pred. No. 0.27; Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32; Oy 114 POALGELEX-PERCENCENCIALENDPROLINSPERRITHESOPELNINFEED 172

一点が

MEDLINE-21154917; PubMed-11230166;

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8
                                                                            652 DG8AALQPILHTVKAG8PSDMPRDSGITDSSVP---SSELSLPLMEGLSTDQTETSSLTE 708
                                                                                                                                        211 LGLADLVCSLRRRMRRRPGPPTSPSIRKQS---GASGHAEGRRTDEEGGREEEG--APAP 265
                                  Gaps
                                                           600 LVLNDVMC------KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600 LVLNDVMC------KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 DGSAALQPLIHTVKAGSPSDWPRDSGIYDSSVP---SSELSLPLMEGLSTDQTETSSLTE 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 PGARA-----GGEGAGSPRRTSRVSG--HTKIPDEDESEVTSSASEKLGR-OPRGRPHRE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the mouse
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bomo sapiens (Ruman).
Bukaryota, Mactazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Rominidae; Bomo.
NCBL_TAXID=9606;
                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
    DB 4; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECTENCE FROM N.A. Elberger J., Soehl G., Willecke K.; Structural and functional diversity of connexin genes in
2.8%; Score 111.5; DB 4; Length 3 28.9%; Pred. No. 0.17; tive 25; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and human genome ";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A14564; CMC93846.1; -
InterPro; IPR000500; Connexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00039; connexin; 1.
PROSITE: PS00407; CONNEXINS_1; UNKNOWN_1.
PROSITE: PS00408; CONNEXINS_2; UNKNOWN_1.
SEQUENCE 370 AA; 40140 MM; CD49F31743A7F7C2 CRC64;
                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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01-0CT-2000 (TIEMBLRel. 15, Last sequence update)
01-DEC-2010 (TIEMBLRel. 19, Last annotation update)
Hypothetical 45.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 111.5; Di
28.9%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                    370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches
                                                                                                                                                                             709 SVSSSGLG-EEPPALPSKLLSSGSCKA 736
                                                                                                                                                                                               709 SVSSSSGLG-EEPPALPSKLLSSGSCKA 736
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLEEL. 19, 01-DEC-2001 (TrEMBLEEL. 19, 01-MAR-2002 (TrEMBLEEL. 20,
                                43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                             Connexin40.1.
 Query Match
Best Local S
Matches 43
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Q9NTU6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 428 Aa; 45443 MW; FA75BACIA3FDB3EE CRC64;
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Matches 70; Conserv
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GenCore version 5.1.4_p5_4578 Copyright (c), 1993 2003 Compugen, Ltd., Sec.	93.5 738 22 AA009952 Bulman 93.7 738 22 AA009958 Human 03.7 726 22 AA004958 Human
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Title: US-09-912-157-2_COPY_36_313 Parfect score: 1515 Sequence: 1 ADTCGWRMKAAARPRICVANRWYMHYALKPVHSPWAGPIR 278	92 6.1 1428 22 ABB65564 9.5 5.9 368 19 ABM41260 8.5 8 1173 ABB9479 5.5 5.6 343 16 AAR73164
Scoring table: BLOSUM62 Gapext 0.5	85.5 5.6 654 22 ANY 8776 85 5.6 313 21 ANY 79996 85 5.6 340 21 AND 3363
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Database : A Geneseq 101002:*	82 5.4 716 15 AAR55200 82 5.4 716 20 AAK42473
1: /sibs/godatc/genesed/genesedp-emb1/AA1981.bAT:* 2: /Sibs2/gogdata/genesed/genesedp-emb1/AA1981.bAT:* 3: /SIDS2/godgata/fenesedy-emb1/AA1981.bAT:*	5.4 716 20 AAW81810 Feline 5.4 716 21 AAW82208 Feline F. 716 21 AAW82208 Feline F. 716 21 AAW875203
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.	2 5.4 716 21 2 5.4 716 21
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	ALIGNMENTS
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geneseqp-embl/	ABB07626;
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1995 /SIDS2/gcgdata/geneseg/genesegp-embl/AA1996	XX DT 20-MAY-2002 (first entry)
genesedp-empl// genesedp-empl//	XX DE Human cytokine receptor, Zcytor18 amino acid sequence.
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* 21: /SIDS2/gcgdata/geneseqp-embl/AA2000.DAT:* 22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* 23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*	XX
Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.	XX OS Homo sapiens
i by analysis of the total score distribu	PN WOZ00208259-A2.
SUMMARIES	PD 31-JAN-2002.
Result Query No. Score Match Length DB ID Description	FF 23-JUL-2001, 2001WO-US23253. XX
1515 100.0 753 23 ABB07626	PR 26-JUL-2000; 2000US-220747P.
1509 99.6 753 23 ABB07627 Human cytokine 1427 94.2 554 23 AAU91330 Human novel sec	PA (2xmo.) 2xmogenetics inc. xx
1427 · 94.2 739 23 ABB07628 Human cytok! 1423 93.9 738 22 AA009904 Human Inter]	PI Presnell SR, Kuestner RE, Gao Z;
Buman Buman Buman	DR WPI; 2002-217048/27. DR N-PSDB; ABA95031, ABA95032.
1423 93.9 738 22 AAU09956 Human 1423 93.9 738 22 AAU09957 Human	AA NA New cytokine receptor polypeptide designated zcytori8, useful for PT inhibiting cell proliferation associated with psoriasis or tumor
	· · · · · · · · · · · · · · · · · · ·

Gao Z;

Presnell SR, Kuestner RE,

-PSDB; ABA95033, ABA95034.

WPI; 2002-217048/27

23-JUL-2001; 2001WO-US23253.

31-JAN-2002.

26-JUL-2000; 72000US-220747P

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The invention relates to an isolated cytokine receptor polypeptide designated Ecytori8. The Zoyfori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhbit call proliferation associated with psoriasis or tumour growth The coll proliferation associated with psoriasis or tumour growth The chinques Zoyfori8 oilgouncleotide probes are useful for in the stay techniques. Zoyfori8 oilgouncleotide probes are useful for in the stay techniques. Zoyfori8 probes and primers can be used to detect and localize Zoyfori8 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in citrosome 3 in which captoris gene resides. The Zoyfori8 polymoriagides can also be used in linkage-based testing of pulmonary alvaolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with the pulmonary alvaolar sequence represents a fundaman Zoyfori8 amino acid sequence.
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and modulating immune system by binding to endogenous zcytor18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine receptor; Ecytori8; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIGMESOPFLAMMRETDYFVKVVPFPSIKNESNYHPRFFRIRACDILLOPDNLACKPFWK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 RIGHESOPPLANKFETDYFVKVYPFSIKNESNYHPFFFRTRACDLLLOPDNIACKPFWR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 2.2e-161;

Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFRYDNCTTYLNPVGRHVIADAQNI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "wild-type Thr is replaced with Met" 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- V750A
/note- "wild-type Val is replaced with Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 NVSPGDYIIELVDD/INTTRKVMHYALKPVHSPWAGPIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 NVSPGDYIIELVDDINTTRKVMHYALKPVHSPWAGPIR 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB07627 standard, Protein; 753 AA.
                                            Claim 1; Page 2; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                      Sequence 753 AA;
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The invention relates to an isolated cytokine receptor polypeptide designated Scytori8. The Scytori8 polypeptides can be expressed by standard_recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Scytori8 in vivo by gene therapy techniques. Ecytori8 oligonucleotide probes are useful for the vivo diagnosis, and the Ecytori8 probes and primers can be used to detect and localize Ecytori8 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Ecytori8 gene resides. The Ecytori8 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial polynocial for fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Ecytori8 variant amino acid sequence.
                                                                                                                                                                                                                          New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand and provided the second scytorial standard and second scytorial standard.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ADTCGWRMRAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ); Score 1509; DB 23; Length 753;
1; Pred. No. 1.1e-160;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 NVSPGDYIIELVDDTNTTRKVWHTALKPVHSPWAGPIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278
                                                                                                                                                                                                                                                                                                                            Disclosure, Page 94-98; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 Sepandard: Protein; 554 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.6%;
Best Local Similarity 99.6%;
Matches 277; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 753 AA;
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Human; secreted protein; cancer; autoimmune disease;

alternation of the

The invention relates to a novel human secreted polypeptide having:

Sequence 90% identical to the polypeptide sequences of LP105, LP061,

C. LP244, LE239(a), LP243(a), LP243(b), LP255, LP028), LP255(b), LP255(b), LP255(b), LP255(a), LP medingitis; encephalitis; neoplasis; trauma; ischaemis; infarctio; pramanis; stroke; cardiovascular ileasase; artherosierosis; saposis; anaemis; rhematoid arthritis; hypothyroidism; allergic response; liver failure; multiple sclerosis; haemorrhage; paranola; obsessive compulaive disporder; autism; panic disorder; learning disability; feeding disorder; sieep pattern disorder; balance; perception; Thi-dependent insulitis; adult respiratory distress syndrome; ARDS. Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease; are Claim 9; Page 171-173; 235pp; English. 11-AUG-2000; 2000US-224642P. 19-OCT-2000; 2000US-241779P. 30-JUL-2001; 2001WO-US21124. Edmonds BT, Micanovic R, (ELIL) LILLY & CO ELI. WPI; 2002-304057/34. N-PSDB; ABK62082. W0200214358-A2. Homo sapiens 21-FEB-2002. disease

Gaps 0; Indels 14; 94.2%: Score 1427; DB 23; Length 554; 95.0%; Pred. No. 1.2e-151; 1ve 0; Mismatches 0; Indels 14; Best Local Similarity 95.0%; Matches 264; Conservative Query Match

Sequence 554 AA;

1 ADTCGWRMKAAARPRICVANEGVGPASRNSGLYNITFRYDNCTTYLMPVGKHVIADAQNI 60

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121 RTGMESOPFLAMKFETDYFVKVVPPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWK 180 181 PRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 240 142 RIGNESQPELNMKFETDIFFVKVVFFPSIKNESNYHPFFFRTRACDLLLQPDNLACKFFFK 201 202. PRNLNISQHGSDMQVSFDHAPHFGFRFFYLHYKLKHBGPFRRKTCKQBQTTETTSCLLQ 261 241 NVSPODITELVODTNITERVHITALKVHSPAGPIR 278 262 NVSPGDYIIELVDDINTTRKVHYALRPVHSPWAGPIR 299 â

RESULT 4

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ABB07628 standard, Protein; 739

ABB07628;

(first entry) 20-MAY-2002 Human cytokine receptor, Zcytor18 splice variant.

EW, Tschang SR, Wang H;

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Ou W,

Cytokine receptor; Zoytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

Homo sapiens.

W0200208259-A2:

31

23-JUL-2001; 2001WO-US23253.

26-JUL-2000; 2000US-220747P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE, Gao Z;

New cytokine receptor polypeptide designated scytori8, useful for inhibiting cell proliferation associated with ps<u>oriasis</u> or tumor growth, and modulating immune system by binding to endogenous scytori8 WPI; 2002-217048/27. N-PSDB; ABA95035, ABA95036.

Claim 1; Page 102-106; 119pp; English.

Ligand

The invention relates to an isolated cytokine receptor polypeptide designated Zcytozi8. The Zcytozi8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psortasis or tumour growth. The encoding nucleic acids are useful for providing Zcytozi8 in vivo by gene therapy techniques. Zcytozi8 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytozi8 probes and primers can be used to detect and localize Zcytozi8 gene expression in tissue samples. The probes are also useful for the detecting gross aberrations in chromosome 3 in which Zcytozi8 gene resides. The Zcytozi8 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with human Zcytozi8 splice variant.

739 AA; Sequence

Indels 14; Length 739; Query Match: 94.2%; Score 1427; DB 23; Best Local Similarity 95.0%; Pred. No. 1.8e-151; Matches 264; Conservative 0; Mismatches 0;

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y 1 ADYCGWRMKAAARPRICOVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNI 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes movel nucleic acids, encoding interleukin (IL) 17 receptor like polypepitides, useful as yaccines and in gene therapy. These have immunomedulatory anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, heptic, anabolic, anorectic, anti-alzheimer's, renai anti-parkinsoinan, anti-ri-satimatic, dermatological, osteopathic, vascular, cotyulashi, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (ILI/TIP) expression. These include, for example immune disorders (e.s. inflammation, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-athelmer's; anti-parkinsonlan; anti-convulsant; anti-asthmatic; dermatological; reaal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                                                              202 PRNIAISQBGSDMQVSFDRAPHNFGFRFFILHYKIKHBGFFRKTCKQBQTTFTTSCILQ 261
                                         TISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFR 120
                                                       121 RTGMESOPFLNMKFETDYFVKVVPPSIKNESNYHPFFPRRACDILLQPDNLACKPFWK 180
                                                                                                                                                 PRNIAISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTGKQEQTTETTSCLLQ 240
                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant rejection), infections (e.g. hepatitis and septicaemia)
hepatitis; anorexia; cachexia; neuronal dysfunction; lung di
bone disease; vascular disorder; eye disorder; cancer; human
                                                                                                                                                                                                                                                                                                                                                                          Human Interleukin 17 (hiL-17) receptor like protein.
                                                                                                                                                                                          241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278
                                                                                                                                                                                                                262 NYSPEDYITELVUDINTTRKVHYALKPYHSPWAGPIR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 152-154; 158pp; English.
                                                                                                                                                                                                                                                                                            AAU09904 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2001; 2001WO-US08678
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28-NOV-2000; 2000US-0724460
                                                                                                                                                                                                                                                                                                                                                14-FEB-2002 (flrst entry)
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N-PSDB; AAS15346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                        AAU09904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jing S;
                                         61
                                                                                                                                                 181
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dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), of dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung-disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. cystema and psorials), kindey disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia, vascular disorders concedistoned and atherosclerosis (e.g. infertility and miscarriage), eye disorders (e.g. infertility and miscarriage), eye disorders (e.g. infertility and miscarriage), eye disorders (e.g. infertility and concedistance in the presence of similar nucleic acids in samples and identify patients needing restoration cherry the printing patients needing restoration of similar nucleic acids in samples and identify patients needing restoration of similar such also be used as antiquens in the production of expression and activity. The arithodies against the proteins and in assays to identify modulators of expression and activity. The arithodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human interleukin: It. (It-17) receptor: like protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin 17; hil-17 receptor like protein; immunomodulatory; anti-diabetic; immunosuppressive; anti-nicobial; hepatic; anabolic; anorectic; anti-alzaeimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cyrostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 ISQYACHDOVAVTILMSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPROLNSSFKR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TGMESQPFILNMKPETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ISQYACHDQVAVTILWSPCALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TGMESOPFLNMKFETDFFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFRKRTCKQEQTTETTSCLLQN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DICGWRMRAAARPRICVANEGVGPASRNSGLYNITERYDNCTTYLMPVGKHVIADAQNIT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 DICGWR------GVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human interleukin 17 (hit-17) receptor like protein substitution #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.9%; Score 1423; DB 22; Length 738; Best Local Similarity 94.9%; Pred. No. 5.2e-151; Matches 263; Conservative (0; Mismatches 0; Indels 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 363. /label- Ser, Thr, Ala, Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU09953 standard; Protein; 738 AA.
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Internation describes unvert decines and in gene therapy: These internation describes useful as vaccines and in gene therapy: These have immunomodulatory, anti-inflammatory, anti-dabetic, anti-microbial, anti-parkinsonian, anti-onvulsant, anti-asthmatic, dermatological, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, anti-parkinsonian, anti-convulsant, anti-ostparic, anti-infertility and stepathic, vascular, cytostatic, anti-leukaemic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, dermatological acids and proteins may be used to prevent and treat diseases associated with internal and creating in disperced include, for example immune disorders (e.g. inflammation, disbetes and contide, for example immune disorders (e.g. inflammation, disbetes and cytic, anti-parking disease and epilepy), weight disorders (e.g. osteoporosis and hypercatcaemia), vascular disorders (e.g. osteoporosis and hypercatcaemia), vascular disorders (e.g. stroke and etheroselerosis, cancers (e.g. lefertility and miscarriage), eye disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal meropathy). The DNA and itse complements may also used as dispense in the production of antiodes against the proteins and antagonists may also be used to every antigens in the production of antiodes against the proteins and antagonists may also be used to expression and artifity and miscariity and misc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention describes novel nucleic acids encoding interleukin (IL) 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treatiby, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page -; 158pp; English.
                                                                                                                                               15-MAR-2001; 2001WO-US08678.
                                                                                                                                                                                                                                                                  16-MAR-2000; 2000US-189816P
28-NOV-2000; 2000US-0724460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611392/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jing S;
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/label- Val, Ile, Met, Leu, Phe, Ala, Nle

Misc-difference 374

WO200168859-A2. 20-SEP-2001. 15-MAR-2001; 2001WO-US08678. 16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

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122 TGMESOPFLNMKFETDFFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACRPFWRP 181
                                                                                                                                                                                                                                                                                                                                                                                          143 TGHESQPFIANKFETDYFVKVVPPPSIKNESNYHPFFFRTRACDLILQPDNIACKPFWFR, 202
                                                                                                                                                                                                                                                                                                                                                                                                              RNINISQEGSDMOVSFDEAPHNFGFRFFTLHFKLKHEGPFKRKTCKQEQTTETTSCLLQN:241
                                                                                                                                                                                                                                                                                                                                                                                                                     103 RMLMISQUESDMQVSEDHAPHNEGFREYLHTKLKHEGPFRRKTCKQEQFTEFTSCLLQN 262
                                                                                                                                                                                                                                                                                                                                                        62 ISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGROCQQLILKDPRQLNSSFRR 121
                                                                                                                                                                                                                                                                                                                 Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                      2 DICGWRMKAAARPRLCYANEGVGPASRNSGLINIIFKYDNCTTYLNPVGKHVIADAQNIT 61
                                                                                                                                                                                                                                                                                                   Query Watch 93.9%; Score 1423; DB 22; Length 738; Best Local Similarity 94.9%; Pred. No. 5.2e-151; Matches 263; Conservative 0; Mismatches 0; Indels 14;
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-incopial; ancectic; anti-inflammatory; anti-incopial; anti-incopial; anti-incopial; anti-oryulant; anti-asthmatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                               Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualiflers
                                                                                                                                                                               AAU09954 standard; Protein; 738 AA.
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Synthetic.
                                                                                                                                                                                                                                                     AAU09954;
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                                                                                                                                                   AAU09954
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Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. laukemia, asthma, diabetes, psoriasis and glaucoma.

WPI; 2001-611392/70.

(AMGE-) AMGEN INC.

Jing S;

Claim 21; Page -; 158pp; English.

738 AA;

Sequence

The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-alzheimer's, renal,
anti-parkinsonian, anti-convulsant, anti-sthmatic, dermatological,
anti-parkinsonian, anti-convulsant, anti-sthmatic, dermatological,
ophthalmological activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
proteins may be used to prevent and treat diseases associated with
containing the polypeptide (ILI/IL)p) expression. These
include, for example immune disorders (e.g. hepatitis and septicaemia),
cusping disorders (e.g. anorexia, cachexia and obesity), neuronal
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
und disorders (e.g. osteoprosis and hypercalcaemia), vascular disorders
confidences and atherosolesis, cancers (e.g. glomerulonephritis),
bone diseases (e.g. osteoprosis and hypercalcaemia), vascular disorders
confidences), reproductive disorders (e.g. infertility and
missarriage), eye, disorders (e.g. disorders (e.g. infertility and
missarriage), eye, disorders (e.g. disorders (e.g. infertility and
missarriage), eye disorders (e.g. disorders (e.g. infertility and
missarriage). miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as disgnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI77ip may also be used as antigens in the production of antibodies against the proteins and in

242 VSPGDXIIELVDDTNTTRKVMHYALKPVHSPWAGDIR 278

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assays to identify modulators of expression and activity. The anti-ILI7rip antibodies and antagonists may also be used to down regulate
                                                  the
                                 expression and activity.

Mote: This sequence is not given in the specification but is based on thuman interleukin 17 (II-17) receptor like protein sequence (AMU09904) and has been created according to information given in claim 21.
                                                                                                                                                                                                                                                                    RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241
                                                                                                                                                                                                                                                                                                                                                                                     203 RNLHISOGGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETJSCLLQN 262
                                                                                                                                                                                                                                                     ISOYACHDOVAVTILMSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPKQLNSSFKR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                             DICGWRMKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 61
                                                                                                                                                                                                             Ruman Interleukin 17 (hIL-17) receptor like protein substitution #5.
                                                                                                                                                                                                                                                                                                            TGMESOPFINMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDILLQPDNIACKPFWKP
                                                                                                                                                                   Indels 14;
                                                                                                                                        Length 738;
                                                                                                                                  93.9%; Score 1423; DB 22;
94.9%; Pred. No. 5.2e-151;
17ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278
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2000US-0724460
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                                                                                                                                                                  Matches 263; Conservative
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Misc-difference 385
                                                                                                                                                Similarity
                                                                                                          738 AA;
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Synthetic.
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                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU09955;
                                                                                                                                    Query Match
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
have 'immunoadulatory, anti-inflammatory, anti-diabetic, anti-microbial,
fumunosuppressive, hepatic, anbolic, anti-alzheimer's, renal,
anti-parkinsonian, anti-anti-anti-anti-alti-alteriality and
correspondance of cytostatic, anti-leukaemic, anti-infertility and
ophthalmological activities; The:IL-17. receptor.like nucleic acids and
protedins may be used to prevent. and treat diseases associated with
propropriate IL-17. receptor like; polypeptide (ILI71p) expression. These
include; for example immune disorders (e.g. inflammation diabetes and
transplant rejection); infections (e.g. hepatitis and septicaemia),
weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
cump disorders (e.g. osteoporosis and obpestly), neuronal
dysfunction (e.g. Alzheimer's disease, Parkinson's disease
(e.g. eczema and psoriasis); kidney disease (e.g. glomerulonephritis),
bone diseases (e.g. osteoporosis and hypercalcaemia), yasulua disorders
(e.g. eczema and atherosclerosis, cancers (e.g. infertility and
breast cancer), reproductive disorders (e.g. infertility and
miscarriage), eye disorders (e.g. infertility and distarriage), eye disorders (e.g. infertility and distarriage). eye disorders (e.g. infertility and distarriage), eye disorders (e.g. infertility and distarriage). eye disorders (e.g. infertility and distarriage). eye disorders (e.g. infertility and distarriage). eye disorders (e.g. infertility and distarriage).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patients needing restorative therapy. The ILI7rip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ILI7rip antibodies and antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22.
                                              Nucleic: acids encoding interleukin 17 receptor like polypeptides, useful for preventing diagnosing and treating, e.g. leukemia, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ISQYACHDQVAVTILWSPGALGIRFLKGFRVILBELKSEGRQCQQLILKDPKQLNSSFKR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGMESOPPLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DTCGWRWKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1423; DB 22; Length 738;
Pred. No. 5.2e-151;
0; Mismatches 0; Indels 14
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                                                                                                                                                         Claim 22; Page -; 158pp; English:
                                                                           useful for preventing, diagnosing diabetes, psoriasis and glaucoma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU09956 standard; Protein; 738 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.9
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       738 AA;
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Matches 2631, Conservative 0, Mismatches 0, Indels 14, Gaps

2 DICGWRMKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPYGKHVIADAQNIT.61 à 윱 ď

à 셤 ð 8 ð

122. TCMESOPFINMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKP 181

203 RNLHISSHGSDMQVSFDHAPHNFGFRFFYLHYKKHGGPFRKRCKGEGTTETTSCLLGN 262

AAU09957 standard; Protein; 738 AA

RESULT, 10

14-FEB-2002 (first entry)

AAU09957;

182 RNINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241

2000

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Interieukin 17: htt-17 receptor like protein; immunomodulatory; intlinitiammatory; anti-diabetic immunosuppressive; anti-microbia; hepatic; anti-microbia; morectic; anti-alzheimer's; anti-parkinsonian; anti-convulant; anti-eakhmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone, disease; vascular; disorder; eye disorder; cancer; human; mutant; mutant; mutant;
Human Interleukin 17 (hir-17) Keceptor like protein substitution #6...
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Homo sapiens. Synthetic.

Location/Qualifiers Misc-difference 515 /label- Asp, Glu

WO200168859-A2

20-SEP-2001.

15-MAR-2001; 2001WO-US08678.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70.

Nucleio acida encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma. diabetes, psoriasis and glaucoma

Claim 23; Page -; 158pp; English.

Interleukin 17; hir-17 receptor like protein; immunomodulatory; anti-diabetic; immunomodulatory; anti-diabetic; immunosuppressive; anti-diabetic; hepatic; anabolic; anorecetic; anti-alzaelmer's anti-parkinsonian; anti-convulsant; anti-asthmatic; dernatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-liceritility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;

Location/Qualiflers

Misc-difference 602

Homo sapiens. Synthetic.

mutein.

Human Interleukin 17 (hIL-17) receptor like protein substitution #7

Treceptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, than the immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The III-Treceptor like muclaic acids and contents may be used to prevent and treat diseases associated with inappropriate II-Treceptor like polypeptide (ILITIP) expression. These include, for example immune disorders (e.g. inflammation, diabetes, and transplant rejection), infections (e.g. inflammation, diabetes, and dystunction (e.g. Alzhelmer's disease, Parkinson's disease and epilepsy), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzhelmer's disease, Parkinson's disease and epilepsy), bune diseases (e.g. osteoporosis and hypercalcemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. infertility and miscarinage), eye disorders (e.g. infertility and alsorders (e.g. antipens in the production of antibodies against the protection and activity. The anti-infilate production of antibodies against the protection and activity miscarinage and antagonists may also be used to down regulate expension and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 23. The invention describes novel nucleic acids encoding interleukin (IL) 17

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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
                                                                                                                                                                                                                                                                                                                                              receptor like polypeptides,
treating, e.g. leukemia, asthma,
                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and
                                                                                                                                                                                      /label- Cys, Ala, Ser
                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page -; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                              diabetes, psoriasis and glaucoma
                                                                                                                                                                                                                                                            16-MAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460.
                                                                                                                                                                                                                                          15-MAR-2001; 2001WO-US08678
                                                                                                                                                                                                                                                                                                                          WPI; 2001-611392/70.
                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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Score 1423; DB 22; Length 738; Pred. No. 5.2e-151;

93.9%; 94.9%;

Query Match Best Local Similarity

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Sequence

anti-parkinsonian, anti-convulanti, ancienti, anti-alizamer's, renal, anti-parkinsonian, anti-convulant, anti-castimatic; dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and optibalmological activities in the III-Treceptor like nucleic acids and corteins may be used to prevent and treat diseases associated with indepropriate II-Treceptor like polypeptide (ILI/IIp) expression. These include, for example immune disorders (e.g., inflammation, diabetes and transplant rejection). Infections (e.g., inflammation, diabetes and dystuction (e.g., Albahamer's disease) parkinson's disease and epithesy), but disorders (e.g., eczema and psoriasis), kidney disease (e.g., glomerulonephritis), bone diseases (e.g., osteoporosis and hypercalcemia), vascular disorders (e.g., stroke and atheroselerosis, cancers (e.g., danfertility and miscarlage), eye disorders (e.g., dancoma and retuinal neuropathy). The miscarlage), eye disorders (e.g., dancoma and retuinal neuropathy). The presence of similar nucleic acids in samples and identify patients needing restoration of antibodies against the proteins and in assays. The III/IIp may also be used as antigens in the production of expression and activity. The assays. anti-ili7rp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 receptor like protein sequence (AAU09904) and has been created according to information given in claim 24. immunosuppressive, hepatic, anabolic, anti-parkinsonian, anti-convulsant, an

888888888888888888888888888888

738, AA; Sequence

Claim 18; Page -; 158pp; English.

ï 143 TGMESQPFLAMKFETDTFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 202 182 RNINISQHGSDMQVSFDHAPHNFGFRFFILHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241 122 TGMESQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 181 0; Indels 14; Gaps 2 DICGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 61 93.9%; Score 1423; DB 22; Length 738; 94.9%; Pred. No. 5.2e-151; tive 0; Mismatches 0; Indels 14; 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299 Best Local Similarity 94.99 Matches 263; Conservative Query Match 8 9 셤 윱 ò 윱 ð õ ð ç

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-incobial; hopetic; anti-orkinsonian; anti-covvulant; anti-orkinsonian; anti-sthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bobe disease; vascular disorder; eye disorder; cancer; human; mutant; mutein. Human Interleukin 17 (hIL-17) receptor like protein substitution #1. į AAU09951 standard; Protein; 738 14-FEB-2002 (first entry) AAU09951; RESULT 11 AAU09951 LD AAU AAC AAU AX AAC AAU AX II 14: AXX BEUM AXX

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, Misc-difference 45 F. Jabel- Gly, Pro or Ala April . The can The High 16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460 15-MAR-2001; 2001WO-US08678 WPI; 2001-611392/70. (AMGE-) AMGEN INC. WO200168859-A2 Homo saplens. Synthetic. 20-SEP-2001. Jing S;

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-inferinces
immunosuppressive, hepatic, anabolic, anti-diabetic, anti-inferinces, renal,
correction, anti-convulsant, anti-diabetic, anti-inferility and
obthalmological activities. The IL-17 receptor like nucleic acids and
cophthalmological activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat disease associated with
controlling to example immune disorders (e.g. inflammation, diabetes and
controlling for example immune disorders (e.g. inflammation, diabetes and
controlling for example immune disorders (e.g. hepatitis and septicamia),
controlling disorders (e.g. orgatic fibrosis, asthma and emplysema), skin disease
correcters (e.g. orgatic fibrosis, asthma and emplysema), skin disease
(e.g. stroke and atherosolerosis and hypercalcamia), vascular disorders
(e.g. stroke and atherosolerosis and hypercalcamia), vascular disorders
(e.g. stroke and atherosolerosis, cancers (e.g. infertility and
miscarriage), eye disorders (e.g. qlaucoma and emplysema),
controllerosolerosis and hypercalcamia), wascular disorders
(e.g. stroke and atherosolerosis, cancers (e.g. infertility and
miscarriage), eye disorders (e.g. qlaucoma and extimal employers
controllerosolerosis and organistic probes to detect and
quantitate the presence of similar nucleic acids in samples and identify
patients needing restorative therapy. The ILI71p may also be used as
controllerosoler Mote: This sequence is not given in the specification but is based on the interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18. expression and activity.

738 AA; Sequence

61 DICGWRMKAAARPRICVANEGVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNIT Query Match 93.5%; Score 1416; DB 22; Length 738; Best Local Similarity 94.6%; Pred. No. 3.2e-150; Matches 262; Conservative .0; Mismatches .1; Indels 14; Query Match N 셤 õ

ISOYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFRR: 121 62 셤 Š

122 TGMESOPFLAMKFETDYFVKVVPPPSIKNESNYHPPFPRTRACDLLLOPDNLACKPFWKP 181

يب زيد نون د S. 5-415

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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-idabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-iparkinsonian, anti-convulsant, anti-astimatic, dermaclogical, osteopathic, vascular, cytostatic anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (ILI)-Ip) expression. These include, for example immune disorders (e.g. inflammation, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-diabetic; immunomodulatory; anti-diabetic; immunomoupressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-lieukaemic; anti-lie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                            143 TGMESQPFLAMKEETDYFVKVVPPPSIKNESNYHPFFFRYRACDILLQDDNIACKPFWFF 202
                                                                                                                                                                                                                                                                                                                                          203 RNIANSQUESDMOVSFDHAPPHAPFERFFFLHYKLKHEGPFKRKTCKQEQTFFTTSCLLON 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
                                                                                                                                                                                                                                                   182 RIGHTSONO SPDHAPHINGERPFILHTRIKHEGPPKRKTCKOBOTTETTSCLLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- Phe, Leu, Val, Ile, Ala, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263.VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278
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28-NOV-2000; 2000US-0724460.
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150 m 190 c 1915
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bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI7rip may also be used as antigens in the production of antibodies against the proteins and in ussays to identify modulators of expression and activity. The anti-ILI7rip antibodies and antagonists may also be used to down regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; pR020005; DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthms; demyelinating disease; destams; demyelinating disease; descentiaginous disorder; transplantation associated disease.
                                                                                                                                                                                                     expression and activity.

Note: This sequence is not given in the specification but is based on the human interleukin 17 (II-II) receptor like protein sequence (AAU09904) and has been created according to information given in claim 19.
glomerulonephritis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ISOTACHDOVAVTILWSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPRQLNSSFKR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TGMESOPFLNMKFETDYFYKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 RNI.NISOHGSDMOVSFDHAPHNFGFRFFILHFKLKHEGPFRRKTCKOEOTTETTSCLLQN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                      37 DYCGWR-------GVGPASRNSGLYNITEKIDNCTITLNPVGKHVIADAQNIT 82
                                                                                                                                                                                                                                                                                                                                                                                                  2 DICGWRMEAARRALCYANEGYGPASRNSGLYNITFKYDNCTTYLMPYGKHYIADAQNIT 61
                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                93.5%; Score 1416; DB 22; Length 738; 94.6%; Pred. No. 3.2e-150; Live 0; Mismatches 1; Indels 14;
(e.g.) eczema and psoriasis), kidney disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asn is N-glycosylated" 56.59 /note= "Asn is N-glycosylated" 113.116 /note= "Asn is N-glycosylated" 147.150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 VSPGDYIJELVDDTNTTRKVMHYALKPVHSPWAGPIR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.24
/note- "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31..34 /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Interleukin 17 receptor, IL-17RH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04958 standard; Protein; 728 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             .. Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                   Sequence 12.738 AA;
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                                                                                                                                                                                                                                                                                                                                    Query Match
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note- "Asn is N-glycosylated"

/note= "Asn is N-glycosylated"

..185

Modified-site

Region

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Agremic lupus erythematosia, Thematoid arthritis, Osteoarthritis, disperante lupus erythematosia, Thematoid arthritis, Osteoarthritis, divenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sigaren's syndrome, systemic sclerosis, arcoidosis, autoimmune haemolyitic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune mediated renal disease, a demyelinating disease, an autoimmune or immune mediated skin disease, contact dermatitis, an aleasic disease of food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; ancectic; anti-larahemer's; anti-parkinsonlan; anti-oravulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                are useful for treating a mammal with an immune related disease, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ACHDOVAVTILWSPGALGIEFLKGFRVILEELKSEGROCOQLILKDPRQLNSSFKRTGME 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 ISQ------HGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 SOPFLAMMETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNLACKPFWKPRNLN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RASASGVPALFVSGEQGVGPASRNSGLINITFKIDNCTTILNFVGKHVIADAQNITISQY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RMKAAARPRICVANE-GVGPASRNSGLINITERYDNCTIYLNPVGKHVIADAQNITISQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Similarity 91.7%; Score 1389; DB 22; Length 728; Similarity 91.6%; Pred, No. 3.5e-147; Conservative 2; Mismatches 8; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buman interleukin 17 (hIL-1) receptor-like protein version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; vascular disorder; eye disorder; cancer; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 ETTSCLLONVSPGDYLIELVDDTNTTRKVMHTALKPVHSPWAGPIR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 ENTSCILONVSPGDYIIELVDDINTTRKVMHYALKPVHSPWAGPIR 288
AAU10602 standard; Protein; 739 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000; 2000US-189816P; 28-NOV-2000; 2000US-0724460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 728 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
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Best Local Simi
Matches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU10602;
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Vandlen RL;
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\$37.00 C

Jing S;

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The invention describes novel nucleic acids encoding interleukin (IL) 17

Treceptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-inferrobial,
immunosuppressive, hepatic, anabolic, anti-diabetic, anti-inferrobial,
contemporation, anti-convulsant, anti-ast#matic, dermatological,
contemporation, anti-convulsant, anti-ast#matic, dermatological,
contemporation anti-convulsant, anti-ast#matic, dermatological,
contemporation anti-convulsant, anti-ast#matic, anti-inferrility and
proteins may be used to prevent and treat diseases associated with
proteins may be used to prevent and treat diseases associated with
contemporate IL-17 receptor like polypeptide (IL)71p) expression. These
include, for example immune disorders (e.g. inflammation, diabetes and
ctransplant rejection), infections (e.g. hepatitis and septicacemia),
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
contemporates (e.g. cystic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasi), kidney disease (e.g. glomerulonephritis),
chous diseases (e.g. osteoporosis and hypercalcaemia), wascular disorders
(e.g. stroke and atheroscierosis, and hypercalcaemia), wascular disorders
(c.g. stroke and atheroscierosis, encores (e.g. leukaemia, myeloma and
miscarriage), eye disorders (e.g. infertility and
miscarriage), eye disorders (e.g. glomerulonephritis)
contemporate the presence of similar nucleic acids in samples and identify
patients needing restorative therapy The III/Trip may also be used as
antigens in the production of antibodies against the proteins and in
assays to identify modulators of expression and activity The
antigens and activity This is the amino acid sequence of human
circle the invention (e.g. the protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Residues 1-288 of this sequence correspond to residues 8-296 of the sequence shown in AAU10601 which is incomplete in the specification.
                                                                                                       Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukaemia, asthma, diabetes, psoriasis and glaucoma .
                                                                                                                                                                                                                            Claim 2; Fig 1; 158pp; English.
                            WPI; 2001-611392/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
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Indels Query Match 91.5%; Score 1386; DB 22; Best Local Similarity 98.8%; Pred. No. 7.7e-147; Matches 25; Conservative 1; Mismatches 2; ä à

739 AA;

Sequence

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KVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWRPRNLNISQHGSDMQVSFDHA 200 81 ALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESQPFLNMKFETDYFV 140 PHNFGFRFFYLHYKLKHEGPFRRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRK 141 201 셤 셤 8 à

AAU11355 standard; Protein; 738 AA. AAU11355; RESULT 15
AAU11355
ID AAU11:
XX
AC AAU11:

셤

(first entry) 26-MAR-2002

Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; gene therapy; protein therapy; immunological disorder.

lomo sapiens.

Location/Qualifiers Misc-difference 25

/note= "Encoded by GIN" /label- Val

WO200190358-A2 .-

29-NOV-2001.

23-MAY-2001; 2001WO-US16767.

24-MAY-2000; 2000US-206862P.

(SCHE) SCHERING CORP.

Sorman DM;

WPI; 2002-106198/14. N-PSDB; AAS18134.

\$ Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response presence of increased protein levels or immunological disorders -

Claim 1; Page 25; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies apable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levely of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRSS polypeptide.

738 AA; Sequence

61 TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFK 120 82 IISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSBGRQXQQLILKDPRQXNSSFR 141 121 RTGMESQPFINMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWK 180 36 ADTCSW------XGVGPASRNSGLXNITFKYDNCTTYLNPVGKHVIADAQNI 81 1 ADTCGWRMKAAARPRICVANEGVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNI 60 15; DB 23; Length 738; Query Match.

88.7%; Score 1343.5; DB 23; Length
Best Local Similarity 90.6%; Pred. No. 4.8e-142;
Matches 252; Conservative 2; Mismatches 9; Indels

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PRNLNISQHGSDMQVSFDHAPHNFGFRFFTLHYKLKHEGPFKRKTCKQEQTTETTSCLLQ 240

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· 1966年 1988年 198

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DD 261 NVSPGDYIIELVDDINTTRKVMHTALKPVBSPWAGPIR 298

Search completed: May 19, 2003, 09:19:57 Job time : 25.9109 secs

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GenCore version 5.1.4_p5_4578 Copyright.(c) 1993 = 2003 Compugen Ltd.	Of protein - protein search, using sw model	Run on: 1, 1, 1, 19, 2003, 09:16:08; Search time 10.263 Seconds (without alignments) 2604.041 Million cell updates/sec	Title: US-09-912-157-2_COPY_36_313 Perfect score: 1515. Sequence: 1 ADTCGWRMKAAARPICVANRVWHYALKPVHSPWAGPIR 278	Scoring table: BLOSUM62. Gapop 10.0, Gapext 0.5	Searched: 283224 seqs, 96134422 residues	Total number of hits satisfying chosen parameters: 283224	Minimum DB seq length; 0 Maximum DB seq length; 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : PIR_73:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	190 kd antigen pre	protein-tyrosine-p	hypothetical prote		gene II protein -	3-1sopropylmalate	alpha-mannosidase-	outer membrane pho	S-antigen - bovine	Iq epsilon chain C	hypothetical prote	ALK-EXO orf133 - B	hypothetical prote			$\boldsymbol{\sigma}$	homeotic protein m	hypothetical prote	hypothetical prote	peroxidase (EC 1.1	teicholc acid blos	hypothetical prote			general secretion	capsid polyprotein	heat shock protein	hypothetical prote
SUMMARIES	a	T42695	H71716	B36182.	T33782	T25186	Z2BPIK	T39210	T51440	C36971.	A28404	EHRT	T25715	T41870	T16225	T37257.	T20487	S70398	A39479	F64171	D64400	S31780	G86740	H85040	T16124	T27433	AE2111	S35961	JC5609	T15626
	8	ď	~	-	~	~	-	~	a	~	~	-	~	~	~	~	~	7	-	~	~	ď	~	~	~	~	~	~	N	7
	Query Match Length	564	341	1462	353	872	421	758	1173	289	404	429	1121	420	461	622	1260	716	320	839	386	363	371	498	236	538	670	2292	377	2102
	Query Match	45.6	6.5	6.3	6.1	6.1	0.9	9	5.8	5.6	9.6	5.6		5.4	5.4	5.4		5.4			5.3	5.3	5.3	5.3		5.3	5.3	5.3	5.2	5.2
	Score	169	66	. 95	93	93	91.5	91.5	88	85.5	85.5	. 85	83	82.5	82.5	82.5	82.5	83	81.5	81.5	81	80.5	80.5	80.5	80.5		80.2	8	79.5	79
	Result No.	-	~	m	+	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	13	50	77	. 22	33	7	52	36	27	78	53

R:Andersson, S.G.E.; Econorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
Nature 396, 133-140, 1998
A:Stitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: H71716

190 kd antigen precursor (scal) RP081 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C; Accession: H71716

RESULT 2

215 LKHEGPFRKRTCKOBOTTETTSCLLONVSPGDIIELVDDTNTTRVMHYALKPVHSPWA 274

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A;Residues: 1-341 <AND> A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14551.1; PID:g386 A;Experimental source: strain Madrid E

A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA

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C;Date: II-Jan-2000	000 #sequence_revision	Wision II-Jan-2000 Ftext	change	11-Jan-2000 -	•
C. Accession: 142	;				
	 E	T, P.: Me	- '	, J.; Wlemann, S	
submitted to the	ο.	e Database, November	er 1999		
	er: 222230;		<i></i>		
A; Accession: T42	T42695	· · · · · · · · · · · · · · · · · · ·	•		
A; Status: preliminary	inary.				
A; Molecule type: mRNA	mRNA				
A; Residues: 1-564	4 CAAA>				
A; Cross-referenc	Cross-references: EMBL:AL133097	2			
Experimental	source: adult tes	testis; clone DKFZp434N1928	4N1928		
C:Genetics:	•			,	
A: Note: DKFZD434N1928	N1928.1				

Query Match	45.64;	Score 691; DB 2	; Length 564;		
Best Local Similarity	llarity 99.28;	Pred. No. 2.9e-56;	•		
	4	smatch	1; Indels	0; Gaps 0;	
	5			•	
Qy 155 HPFFFR	TRACDILIAPDNIACE	HPFFFRTRACDLLLQPDNLACKPFWKPRNLNISOHGSDMQVSFDHAPHNFGFRFFYLHYK	VSFDHAPHNFGFRFI	YLHYK 214	
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Db 1 RPFFFR	TRACDLLLOPDNLACE	HPPFFRTRACDLLLOPDNLACKPFWKPRNLNISQBGSDMQVSFDHAPHNFGFRFFYLHYR	VSFDHAPHNEGFRF	YLHYR 60	

Db 259 NDGNDPIQKFFITLQEAGTPTFTFHKDFINGSHTSYILDHFKPNTTYFLRIVGKNSIGNG 318	OY 58QNITISOYACHDOVAVILMSPGALG-IEFLKGFRVILEEL 97	98 KSECROCOQLILKDPROLMSSFKRTGMESOPPLANGEFTDIFVKVPPPSIKNESNTHPP	DD 5/3 - SGEDKLKTATDYE 408 QY 158 FERTRACDLLIQPDNLACKPEW	409 -FRVRACSDLTKTCGP-WSENVNGTTWDGVATRPINLSIQCHHDNVTRGNSIAINW 198 DHAPHNFGFRFFYLHYKLKHEGPFRRKTCKQEGTTETTSCLLQNVSPG-DY	248	Db 518 TVTVSAITRHKKNGEPATGSCLAPVSTP: 545 RESULT 4	T33782 hypothetical protein C39F7.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000	tober 1998	- G	A.Residues: 1-53-748G> A.Cross-references: EMED:AR101310; PIDN:AAC69214.1; GSPDB:GN00023; CESP:C39F7.5 A.Experimental source: strain Bristol N2; clone C39F7	V.Goner.CSS:C39F7.5 A.Map position: 5 A.Introns: 14/2; 46/3; 224/1 C.Sunarfamily: Cananahitit a lagana humothatical protein G3007 5	rength 55: Inde	GROCOLLIKOPKOLNSSFKRTGMESOPFLNMKFETDYFVKVV 143	26 GIRSARNVIRATSRIKFSFRRKSSTRDGTRPFBELIKSWPVQDLMILLAEFEADSKILL	OY 144 PEPSITABENTARODIAGENERMENT	OY 187 -SOHGSDMQVSFDHAPHNFGFRFFFLHYKLKHEGFFKKTCKQEG 230		RESULT 5 725186 hypothetical protein 723F6.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 31-Jan-2000	C;Accession: 725186
sca2, RP081 (5.5%; Score 99; Match	Pred. No. 0.21; 35;::Mismatches 120; Indels:: 88; Ga	22 23	OY 59	QY 98 KSEĞRQCQQLILKDPKQLNSSF-KRTGMESQPFLANKRENGFFVKVVPFPSIKNES 152 DD 158 TSYGHNYIKNKSKNLANKIIGKYQNNNFQTLLNYKYRTKYNLHFIPSIGFKTDYSRAS 214	OY 153 NYHPFFRTRACDIALQPDNLACKPFWKPRNLNISQHGSDMQVSFDH 199 1	QY 200 APHNEGERETILEYKLKHEGPEKRTCKQEQTIETSCLLQNVSPEDYIIELVDDTNTR 259 DD 264NIERHENNKNIYVNAKATEKKQTLQETIIIPKQPKLGINIGNNILMSIKNINVLL 318	OY 260 KVMHYALKPVHS 271 Db 319 EYNYTHKKYHS 330		protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type PrP69D precursor - fruit fly (NiAternate names: protein-tyrosine-phosphatase DPTP C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Cbte: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 10.Sep-1999	R.Streull, M.; Krueger, N.X.; Tsal, A.Y.M.; Salto, H. Proc. Netl. Acad. Scl. 10.5.A. 86, 8698—8702, 1989 A. Ittle: A. family of receptor-linked profess through the physics of humans and process	1		A;Cross references: FlyBase:FBgn0014007 C;Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III phosphatase homology	C; Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane F: 1-28 Domain: slynal sequence Fstatus predicted (SIG) F: 29-1462/Product: protein-transfer-and-phosphatase construction protein-transfer-and-phosphatase construc	F:39-806/Pomain: extracellular fetation predicted CEXT> F:38-14/Pomain: immunoglobulin homology <imi> F:34-12/Pomain: immunoglobulin homology <imi></imi></imi>	F;807-823/Domain: transmembrane fatatus predicted <tmn> F;824-1462/Domain: intracellular fatatus predicted <int> F;824-1462/Domain: protein-tyrosine-phosphatase homology <ptp1></ptp1></int></tmn>	F:1413-143//Domain: profeden-tyrosine-phosphatase homology <ptp2> F:45-112,154-214/Disulfide bonds: fatatus predicted F:1037/Active site: Cys (phosphocysteine intermediate) fatatus predicted F:1037/Active site: Substrate phosphate (Arg) fatatus predicted F:13103/Active site: Cys (phosphocysteine intermediate) fatatus predicted F:1397/Binding site: Substrate phosphate (Arg) fatatus predicted</ptp2>	Query Match 6.3%; Score 95; DB 1; Length 1462; Best Local Similarity 20.4%; Pred. No. 3.5; Matches 67; Conservative 45; Mismatches 100; Indels 116; Gaps 18;	QY 20 NEGVGPASRNSGLTNITEKIDNGTTILNPVGRHVIADA 57

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alpha-mannosidase-like protein - Arabidopsis thaliana
N;Alternate names: protein F2614_70
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51440
C;Accession: T51440
S;Sato, S; Nakamura, T; Kaneko, T; Kato, T; Asamizu, E; Kotani, H; Tabata, S;
Submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Readidues: 1758 - 400D>
A, Status Freferences: EMBL: 899262; PIDN: CAB16402.1; GSPDB: GN00066; SPDB: SPAC9E9.03
A, Experimental source: strain 972h-; cosmid c9E9
                                                                                                                                                                                                                                                                                                   DD 1 2 3 17 PSSVIKSGNISNSKANRIPGPIRRLVNEG-TDNVAQTMERTTFWRSLKELTSVGLSKAQL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 -----VAGSV--SSGSAGIPKFTVVEGIAAPLPMANVDTDKII---PKOFLKTIKRTG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 mesqpflnmkfetdyfvvvpfpsiknesnyhpfffrtracdlllopdnlackpfwkprn 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 LGQFAFYEIRYDAD -- GKEIP-DEVLNREPY ------RHATVLVAHDNEGC------- 615
258 GLPRKFFDIVKTQDNIESGSFNLIC-DL#KKSFKDLFDAFKGSDMNVTDDSKVTDALINN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 QYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 -AAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHV-----IADAQNITIS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.0%; Score 91.5; DB 2; Length 75%; Best Local Similarity 24.6%; Pred. No. 3.1; Matches 51%; Conservative 22; Mismatches 85; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone F2G14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: iron-responsive element-binding protein
                                                                                                                                                                                     376 MALSTDINAVPLYQMINVDFSQQYPEWYVEPV 407
                                                                                                                           2 240.QNVSPGDYIIELVDDTNT--TRKVMHYALKPV (269%)
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A; Residues: 1-1173 <SAT>
A; Cross-references: EMBL:AL391146
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A;Gene: leu2; SPDB:SPAC9E9.03
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A;Introns: 192/3; 242/3; 253/3
A;Note: F2G14_70
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Mol. Biol. 181, 739, 1985
TILLs: Nucleotide sequence and genetic organization of the genome of the N-specific fi
Reference number: A92912; MJID:85160831; PMID:3981635
                                                                                                                                                                                                                                                                    A;Nap position: 4
A;Introns: "74/3; 170/1; 441/1; 662/2; 727/3
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                A) Residues: 1.872 CMILS
A) CTOSE-references: EMBL: 883127; PIDN: CABO5631.1; GSPDB: GN00022; CESP:T33F6.4
A) Experimental source: clone T23F6
C) Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 E---FLERKRYGDLV------GFGEVQEYTA 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 ILEELKSEGRQCQQLILKDPRQLNSSFKRTGWESQPFLNWKFETDYFVKVVPFPSIKNES 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 NYHPFFFRTRACDILLIOPDNIACKPFWKPRNINISOHGSDMOVSFDHAPHNFGFRFFY-- 210
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Best Local Similarity 21.4%; Pred. No. 1.4;
Matches 71; Conservative 44; Mismatches 98; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AAAMPEL----IDVTFSAKVAND 154
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                                                                                                                                                                                                                                                                                                                                                 Query Match
6.1%; Score 93; DB 2; Length 872;
Best Local Similarity 22.7%; Pred. No. 2.7;
Matches 40; Conservative 27; Mismatches 63; Indels 46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 ------LHYKLKH-----EGPFKRKTCKQBQTTETTSCLLQNV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:K02750; NID:g14942; PIDN:CAA26067.1; PID:g14943; Comment: The gene II protein is required for DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700. FDAKTALKDMOGELLDGHSLELKISHRENADKGALKRKEVROKEOGECTKLLVRNL 755
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                                                                                             ;Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                   sútmitted to the EMBL Data Library, November 1996
A; Réferènce number: £19992
A; Accession: T25186
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Residues: 1-421 <PEE>
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Molecule type: protein

2.52,56.66,74-96;103-117;132-165;176-226;251-257;299-308;322-333;355-367;

Reakidue; 2.53,56.66;74-96;103-117;132-165;176-226;251-257;299-308;322-333;355-367;

Ramki, K.; Takahashi, T.; Sakuragi, S.; Matsubara; K..

Lochem. Blophys. Res. Commun. 142, 904-910, 1987

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Reference number: A25826; MUID:87156714; PMID:2950857

Accession: A25826
                         C; Accession: B28404; A28404; A25826; A23619; S02144; S51073; I46054.
R; Shinohara, T.; Dietzschold, B.; Craft, C.M.; Wistow, G.; Early, J.J.; Donoso, L.A.; Proc; Natl. Acad. Sci. Cu.S. 4; 6975-6979, 1997.
A; Ittle: Primary and secondary structure of bovine retinal S antigen (48-kba protein)
A; Reference number: A28404; MUID:88041034; PMID:3478675
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Biol. Chem. 269; 15407-15410, 1994
Title: A splice variant of arrestin. Molecular cloning and localization in bowine r
Reference number: A54008; MUID:94253112; PMID:7515057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: protein
Fesidues: 5-13;198-229 <TSD>
Kleselbach, T.; Irrgang, K.D.; Rueppel, H.
Ir. J. Blochem. 226, 87-97, 1994
Title: A segment corresponding to amino acids Vall70-Arg182 of bovine arrestin is c
Reference number: S51073; MUID:95045604; PMID:7957262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
Residues: 166-404 (MIS>
Cross-references: GB x03454; NID:975; PIDN:CAA27179.1; PID:976
Cross-references: GB x03454; NID:975; PIDN:CAA27179.1; PID:976
Cochim. Biophys. Acta 994, 191-193, 1989
Title: The amino acid sequence of S-antigen: N-terminus and uveitogenic peptides.
Reference number: S02144; NUID:89088273; PMID:2910351
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C; Superfamily: arrestin
E; F: 404/Product: S-antigen, long form #status predicted CMAI>
E; S-404/Product: S-antigen, short form #status predicted CMAI>
E; S-404/Product: S-antigen, short form #status predicted CMAI>
E; I/VO-182/Region: Indopsin binding
E; I/VO-182/Region: Indopsin binding
E; I/Modified site: blocked amino.emd (Met) #status experimental
E; 128-143/Disulfide bonds: #Status predicted
E; 228, 271/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 PAPNHYIPKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDP----ELVKGKRVYV- 59
                                                                                                                                                                                                                                                             Cross-references: GB:J02955; NID:g162671; PIDN:AAA30378.1; PID:g162672
Accession: A28404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 PVGKHV----IADAONITI----SQTACH-----DQVAVTILWSPGALGIEFLKGFRVILE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ woolecule type: mRNN Residues 1.369, A <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 85.5% DB 2; 20.6%; Pred. No. 4.9; tive 32; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: protein
Residues: 170-182 <KIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 61; Conserve
                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1-404 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: 146054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane phospholipase A (EC 3.1.1.-) precursor - Proteus vulgaris Cispecies: Proteus vulgaris Cispecies: Proteus vulgaris Cispecies: Proteus vulgaris Cibace: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999 C;Accession: C36971; S40130 E., van Boxtel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm A.Bacteriol. 176, 861-870, 1994 A.Fille: Molecular characterization of enterobacterial pldA genes encoding outer membran A.Fattle: Molecular characterization of enterobacterial pldA genes encoding outer membran A.Fattle: Molecular Characterization (S6971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Cross-references: EMBL:X76902; NID:g436889; PIDN:CAA54224.1; PID:g436890
A/Note: authors translated the codon GAG for residue 74 as Gly and CGA for residue 115
                                                                                      ;
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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N:Alternate names: 48K rhodopsin-binding protein; arrestin
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 KPFWKPRNLNISQHGSDMQ-VSFDHAPHNFGFRFFYLHYKLKHBGPFKRKTC----- 226
                                                                                                                                                                         62 ISQIACHDQV-AVTILWSPGALGIRFLKGFRVI-LEELKSEGRQCQQLILKDPRQLNSSF 119
                                                                                                                                                                                                                                                                                                386 ERALKLIDOYRKKSTLYRTHTLIPIGDDPRYISIDEAEAQFRYTQHIF-----434
                                                                                                                                                                                                                                                                                                                                                                                                          435 -- DHINSNPSLANAEAKEGILEDTFRIVEREADRVNTSRPOGFVGSGOVVGFPSLSGDFFTY 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SDLNKKAI---ESYNWSDNANKDEVKFOLSLAFPLWR-GILGDNSLLGASYTORSWWOLS 121
                                                                                                                                   3 TCGWRWKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLMPVGKH-VIADAQNIT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 NPVGKHVIADAQNITISQYACHDQVAVTI-----LMSPGALGIEFLKGFRVILE---ELK 98
                                                                            38; Mismatches 102; Indels 132;
                   5.8%; Score 88; DB 2; Length 1173;
Similarity 21.8%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%; Score 85.5; DB 2; Length 289. 26.5%; Pred. No. 3.1; atlive 16; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 KOEGITETTSCLLONVSPGDYIJELVDDTNTTRKVMHYALKPVHSPWA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 EKEKSDQ-----SPSFFEAEQMRS-----KYDARPVHKPIA 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 SEGROCOQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: pldA
C;Superfamily: bacterial phospholipase Al
C;Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                          120 KRIGHESOPFLN--MKFET--DYF----
                                                                            76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
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Matches 43; Conserv
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A; Molecule type: DNA
A; Residues: 1-289 <BRO>
Query Match
                                                                                Matches
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:52:40 2003 us-09-912-157-2_	copy_36_313.rpr
DD60	RESULT 12 T35715
149	hypothetical protein F19F10.11a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
189 BGSDMQVSFDHAPHNFGFREFYLHYKIK	C; Accession: 725715 R; Relien, J; Hamalley, P. Submitted to the EMEL Data Library, April 1997 A; Description: The sequence of C. elegans cosmid F19F10.
ATHSTDVEEDKIPKKSSVRLLIRKVQH HEGPPKRKTCKQEQTTETTSC	number: £20073 : T25715 :eliminary; translated from GB/
	A.Molecule type: DNA A.Residues: 1-1121 <kel> A.Cross-references: EMBL:U97005; PIDN:AAB52289.1; GSPDB:GN00023; CESP:F19F10.11a A.Experimental source: strain Bristol N2: clone F19F10</kel>
RESULT 11 EHRT IG epsilon chain C region - rat	10.11a
C.Species. Actua Duregius (MOJMA) IC.) C.Species. 17-Dec-1982 * Sequence_revision 17-Dec-1982 * text_change 16-Jul-1999 C.Accession: A93442; A90937; A02143 R.Hellman, E.: Pettersson, U.: Engstrom, A.: Karlason, T.: Rennich H	A;Introns: 19/3; 54/2; 87/2; 120/2; 152/2; 181/2; 337/2; 432/2; 456/3; 833/2; 858/2 Query Match 5.5%; Score 83; DB 2; Length 1121;
Nucleic Acids Res. 10, 6041-6049, 1982, A.Title: Structure and evolution of the heavy chain from rat immunoglobulin E.	Matches 50; Conservative 29; Mismatches 79; Indels 48; Ga
A. Accession: A9344.2 A. Accession: A9444.2 A. Poblecule type: mRNA A. Poplecule type: mRNA	OY 79 POALOIRELKGERVILLEBIKSEROCOQLILEDROROLNISSERTOHESPEP-INNHEFFI 36 ~
A; Experimental source: strain LOU/c/Msl, immunocytoma IR2 R; Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.	137DYEV-KVYPFPSIKNESNYHPFFFR-TRACDLLLQPDNLACKPFWKERNL:
DAR 1, 353-1451, 1984 A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, i A;Reference number: A90337; MUID:83182019; PMID:6820340	DD 823 VEEDEETFVEREIPAPSLSPPAEILEKPKWFRKTSKYDAKIAALKKDFKPAKFVKVFVST 882 Qy 185 NISQHGSDMQVSFDHAAPHNFGFRFYLHYKLKHBGPFKRRTCKQBQTTETTSCLLQNVSP 244
A;Cortents: myeloma IR162 A;Accession: A90937 A;Molecule type: mRNA	DD 883 SCVQCGTP
A; Residues: N',169-307,'L',309-342 <kin> C; Complex: No immunoglobulib heterotetramer subunit consists of two identical light (kap</kin>	245 GDYIIELVDDTNTTRKVMHYALKPVH
ssociate	DD 916 GAIPLELTPPI-FURKAIFFCLEHMH 940
F:19-80/Domain: immunoglobulin homology <imi>F:118-186/Domain: immunoglobulin homology <imi>F:118-23-291/Domain: immunoglobulin homology <imi>F:223-291/Domain: immuno</imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi></imi>	[3]
F;327-396/Domain: immunoglobulin homology CIM4> F;327-396/Domain: immunoglobulin homology CIM4> F;46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicte	
ngth 429;	C;Date: (0.2 bec. 1999 # sequence_revision 03-Dec-1999 #text_change 21-Jul-2000 C;Accession: T41870 R;Gomi, S.; Majima, K.; Maeda, S.
QY 56 DAQNITISQYACHDQVAVILWSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDP 112	J. Gen. Virol. 80, 1373-1337, 1999 A.Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus. A.Reference number: 22020; MUID:99281911; PMID:10355780
115 NAFHSTIGLYCFVYGHIONDVSIHWLADDRKIYETHAQNVLIKEE	elimin PPe: D
QY LLS KOLMSSFKRYGMESQPFLANKFETDYFVRVVPFPSIKNESNTHPFFFRTRACD 165 : :: : : :	A; Residues: 1-420 <kam> A; Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63799.1; PID:g3745952 A; Experimental source: isolate T3</kam>
OY 166 LLLQDDNLACKPFWRPRNLNISOHGSDMQVSFDHAPHN- 203 Db 209 TPVI.PDSPDIJVPRVTPRT.FCT.VI.DI.ESEPHTTTTMADPBFFFFFTCSSCOORGEL-UNA 266	C; Supertize alk exo C; Superfamily: OpWNPV alkaline exonuclease
204	Query Match 5.4%; Score 82.5; DB 2; Length 420; Best Local Similarity 21.2%; Pred. No. 9.8; Matches 48; Conservative 27; Mismatches 74; Indels 77; Gaps 11;
230	OY 48 PVGKHVIADAQNITISQYACHDQVAVTILMSPGALGIEFLKGFRVILEEL 97
DD 34/ ADAKTLICLIONFFFEDISVQMLQDSKLIPKSQHSYTTPL 366	QY 90 KSEGRQCQQLILKDPRQLNSSFRRTGMESQPFLNMKFETDT-FVKVVPFPSIK 149

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Db 266 AYENSHCERYQCADKRRLSFRMESCHENYSQQRIDAMYDRGIYLDYGHLKCAYCHDFS 323	A; Molecule type: DNA A: Residues: 1-623 < CTA>
OY, 150 NESNYHPPEFFTRACDILLOPDNIACKPEWKPRNIALSOHGSDMOVSFDHAP 201	erences
Ä	C;Genetics: A:Gene: R0201:1
	A;Map position: V A;Introns: 38/2; 77/1; 191/2; 280/3; 308/2; 335/3; 472/3; 587/3
YLTHIGTLRTFCCG	Query Match 5.4%; Score 82.5; DB 2; Length 622;
RESULT 14	9; Conservative 31; Mi
hypothetical protein Files.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans	QY 18 VANEGY-GPASRNSGINITFKYDNCTTYLMPVGKHVIADAQNITISQYACHDQVAVT 74
C; Date: 20-Sep-1999 feequence_revision 20-Sep-1999 ftext_change 20-Sep-1999 C; Accession: T16225	IINQGYETPASGRNOLENLTEGFKYIKVDMNNISSSKYASKD-
Ribu, Z. Subaltred to the EMBL Data Library, April 1996	Oy 75 ILWSPGALGIEFLKGFRVILEELKSEGRQCQQL-ILKDFRQLANSFKR 121
A) Reference rumber: 218481	180 SMWEIIFFTVIKIDSVQHCKEFDIDSI EKKINGEREITER MELCEEB
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Wolecule type: DNA	D 229 AGRRNQGDIMKYTEQELOSCANDLHDYYVNEWNNSRYELEUTQLIKIN 276
A; Residues: 1-461 <du2> A; Cross-references: EMBL:U55856; NID:g1280154; PID:g1280157; PIDN:AAA98022.1; GSPDB:GN00</du2>	OY 172 NLACKPFWKPR-NLNISQBGSDMQVSFDH 199
A:Experimental source: strain Bristol N2; clone F3IE8 C;Genetics: A:Gene: CESP:F31E8.5	: : : : : : Db 277 QALQKGIWESRPKWELGRVFWVLKIEPSH 305
A;Map position: 2 A;Introns: 30/1; 42/2; 78/2; 148/3; 185/2; 245/3; 302/3; 361/1; 388/3; 432/3	Search completed: May 19, 2003, 09:25:13
18; Score 82.5; DB 2; 18; Pred. No. 11;	JOD Time : 15.263 Secs
Matches 59; Conservative 39; Mismatches 103; Indels 105; Gaps 14;	
29 NSGLYNITEKEDN-C-TTYLNPVGKHVIADAONITISQIACHD	
62 INGFFHISFMPPNICHAITVCPVKKDNITDAHNLAIAESTCEERTVKIT	
UY 70 -QVAVIIIMSPOALGIEELAGENVILEELKSEGRACQQLIIKOPRQIASSERRTGRESQP 128 12. GOSEVRKIWARRRIEFIIDDOGISKVHVISKSPERRIDEFTSAVDRGETV 170	
129 FLANKFETDYFVKVVPFPSIKNE - SNYHPFFFRTRACDLLLQPDNIAC	
Db 171 ANNLK-DTDLILITNSRMCQVNKIGSTYFPLFRKAVQKDTKGLFFKWLND 219	C. C
OY 187 SQUGSDWQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRYTCK	
Db 220 RRTQVATDYLPPVKEKDAKKSIDLLAYLKTLDHKNGVL 257	
TTRKVMHYALK : !	
DD 230 ARREATLESVOOLASAGRERANDRELINAALERKVSVKIIPHIPRUMHVSNAIRAFILS 31/	
hypothetical protein R02D1.1 - Caenorhabditis elegans C; Specieles: Caenorhabditis elegans C:nate: 03-poc-1000 fearmone rentsion 03-poc-1000 feart	
C.Accession: T37257 C.Accession: T37257 R.Clarke, K.: David, M.	
submitted to the EMBL Data Library, June 1999 A: Description: The sequence of C. elegans cosmid R02D1. A: Reference number: 21650	
A; Accession: T37257 A; Status: preliminary; translated from GB/EMBL/DDBJ	
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xenopus lae klebsiella drosophila human papil

091684 y 937078 y 044220 c 927558 p 905129 p 096117 p p 17181 p 029753 e

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Scoring table:

Searched:

Title: Perfect score:

Sequence:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pangrustacea; Hexapoda;

Eukaryota; Perygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Fortein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-
tyrosine-phosphate phosphohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine + phosphate.
-- SUBCELLGAR LOCATION: Type I membrane protein.
-- SIMILARITY: CONTAÎNS 2 ÎNMUNOGLOBULIN-LÎKE C2-TYPE DOMAÎNS.
-- SIMILARITY: CONTAÎNS 2 FIBRONECTÎN TYPE IÎI-LÎKE DOMAÎNS.
-- SÎMILARITY: CONTAÎNS 2 PROTEÎN-TROSÎNE PHOSPHATAŞE DOMAÎNS.
                                                                     SORC KLEPN
CCB1_DROAC
V12_HPV41
KPCG_HUMAN
CHAC_HUMAN
INR1_HUMAN
                                                                                                                                                                                                                                                                          . PRT; 1462 AA.
                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P18052; IrFO.
FlyBase; FBGN0014007; Ptp69D.
FlyBase; FBGN0014007; Ptp69D.
InterPro; IPR003961; FW.III.
InterPro; IPR003066; Ig_MG.
InterPro; IPR003509; Ig_Like,
InterPro; IPR000360; Ig_like,
InterPro; IPR000360; IT_IPPD.
InterPro; IPR000242; TYT_PP.
PHK_SCHPO
EX5C_BUCAI
EXON_NPVAC
:ICN2_LACLA
DPG1_XENLA
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                                                                                                                                                                                                                   EMBL; M27699; AAA28842.1; -. PIR; B36182; B36182.
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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haemophilus
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schizosacch
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rattus norv
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candida alb
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                                                                                           May 19, 2003, 09:08;53 ; Search time 5.64467 Seconds (Without alignments) 2042.709 Million cell updates/sec
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P03660 bacterloph
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           US-09-912-157-2_COPF_36_313
1515
1. ADTCGWRKGAAARPRICVAN.....RKVWHYALKPVHSPKAGPIR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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P34765
P45182
           Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                   . protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTP6_DROME
VG2_BPIKE
LEU2_SCHPO
PA1_PROVU
ARRS_BOVIN
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MCE1_CANAL
ZP2_FELCA
MEC3_CAEVU
TDDB_HAEIN
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TBX5_HUMAN
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MY10_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMBB_TEAST
CC25_YEAST
MEC3_CAEEL
LEU2_CANMA
UTRO_HUMAN
MEC3_CAEBR.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match
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Database :

Result No.

Pfam, PF00041; fn3; 3.
Pfam; PF00047; 1g; 2.
Pfam; PF00102; X_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE.

mus musculu

bacteriopha

LYCA_BPCP7

333335555555555555555555

'BX5_MOUSE

vibrio chol encephalomy

human herpe

24443 **29kte6**

SM00060; FN3; 3. SM00410; IG_like; 1. SM00408; IGC2; 1.

SMART; SMART; SMART;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDITINE-85160831; PubMed-3981635; Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H., Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H., Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H., Willeotide sequence and genetic organization of the genome of specific filamentous pages M13, fd and fil"; the genome of J. Wol. Biol. 181:27-39(1985).

-I. FUNCTION OF THE GENE X. PROTEIN IS REQUIRED FOR DNA REPLICATION. THE FUNCTION OF THE GENE X. PROTEIN IS UNKNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RACDLLLQPD-----NLACKPFWKP--RNLNISQHGSDMQV----SFDHAPHN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 GLPRKPFDIVKYQDNYESGSFULIC-DLWKKSFKDLFDAFKGSDMNVYDDSKYDALINN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 FGF-----ETTS----CLL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 QVA-----------VTILWSPGALGIEFLKGFRVILEELKSEGRQCQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 QLILKDPRQLN-SSFRRTGME--SQPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRT- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 FSSVTKSGNISNSKANRLFGFTRRLVNEG-YDNVAQTMERTTFWRSLKELTSVGLSKAQL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 HIANQVISFLRNVSNGQTKKTRALDYETTVMWNEGS-----RHRTLVAYLKHHEVQAQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 91.5; DB 1; Length 421; 21.4%; Pred. No. 0.47; tive 44; Mismatches 98; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626AC1FDDF4E5215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA replication, Alternative initiation.
CHAIN 1 421 GENE II PROTEIN.
301 421 GENE X PROTEIN.
INIT_MET 301 301 FOR GENE X PROTEIN.
                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Gene II protein [Contains: Gene I protein].
                                                                                                                                                                                                                                                                                                                                   Viruses; sspNA viruses; Inoviridae; Inovirus NCBI_taxID-10867;
                                               421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 QNVSPGDYIIELVDDTNT--TRKVMHTALKPV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 MALSTDANAVPLVQMINVDFSQQYPEWYVEPV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X02139; CAA26067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X02139; CAA26068.1; -. PIR; A04265; Z2BPIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.4%
Matches 71; Conservative
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-85160831; Peeters B.P.H., Pei
                                                                                                                                                                                                                                                                                                           Bacterlophage IKe.
                                               VG2_BPIKE
                                                                                                                                                                                                                                                                    II AND X.
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       VG2_BPIKE
AC POT 21-JU
VG2_BPIKE
DPT 21-JU
VG3_B
DPT 21-JU
VG1_B
DPT 16-OC
VITUS
VG1_B
DPT VG1_B
DPT VG1_B
DPT CG1_B
DPT C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 QPTQTPQGITTLSY---DPIFIPKVETTGSTASTITTGWNPPPPDLIDYIQYYELIVSE- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 KSEGROCOOLIIKDPKOLNSSFKRTGMESOPFLNMKFETDYFVKVVPFPSIKNESNYHPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEGVGPASR-----NSGLYNITFKYD------NCTTYLNPVGKHVIADA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----QNITISQYACHDQV-----AVTILWSPGALG-IEFLKGFRVILEEL 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 20.4%; Pred. No. 1;
Matches 67; Conservative 45; Mismatches 100; Indels 116;
                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE DPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN-TYROSINI PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENT
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                                                                                                              Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; F8091D69E88230EB CRC64;
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE C2-TYPE DOMAIN 1 IG-LIKE C2-TYPE DOMAIN 2
                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                             lobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95;
PS00383; TYR_PHOSPHATASE_1; 2
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 TVTVSAITRHKKNGEPATGSCLMPVSTP
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                                                                                                                                             Cell adhesion; Immunog
                                                                                                              ydrolase; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1462 AA;
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                                                                          ROSITE
                                                                                                                                                                                         SIGNAL
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NAME OF THE PARTY 
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Ź 758 O14289; 15-JUL-1998 (Rel. 36, Created) LEU2_SCHPO ID LEU2_SCHPO

RESULT 2

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RADDINES. 1988 01. FURNES. 1593501.

RA MOOD V. GWIlliam R., Rajandes J., Basham D., Bowman S., Bgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Radios S., Chillingworth T., Churcher C.M., Colling M., Connor R., Croin A., Davis P., Feltwell T., Fraser A., Collins M., Connor R., Croin B., Bowith P., Feltwell T., Fraser A., Bentles S., Goble A., Hamilia, N., Harris D., Hidalgo J., Hodgson G., Hones L., Jones M., Leather S., McDonald S., McLean J., McDonay P., Wolle S., Mcmes M., Leather S., McDonald S., McLean J., Ramsonds M., Squares S., Stevens K., Sharp S., Aller S., Ruther S., Stevens K., Sharp S., Relton J., Stumonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Rodderd J., Volckaert G., Aert R., Robben J., Grwnoprez B., Moodward J., Volckaert G., Aert R., Robben J., Grwnoprez B., Moddward J., Volckaert G., Aert R., Robben J., Grwnoprez B., Moddward J., Volckaert G., Aert R., Robben J., Grwnoprez B., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert R., Polt T.M., Roffen W., Cadleu E., Dreano S., Cloux S., Lelaure V., Mottier S., Amblert R., Polt T.M., Goffen J., Jimenez J., Sanchez M., Gelzue B., Poraburg S., Locas M., Rocher W., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gelzue S., Karstrong J., Forsburg S.L., The genome sequence of Schizosaccharomyces pombe.", The Grand S., Charland C., There F., H., The Grand S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isopropylmalate.
-!- PATHWAY: Leucine blosynthesis; second step.
-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWIss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not, removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
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SIMILARITY).
15 UNI 1998 (Rel. 36, Last sequence update)
15-UNI-2002 (Rel. 41, Last annotation update)
3 isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- CATALITIC ACTIVITY: 2-isopropylmaleate + H(2)0 - 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
(BY
                                                                                                                    orm.zus.vs.
Schizoscharomyces pombe (Flasion yeast).
Bukaryotes, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leucine blosynthesis; Lyase; Iron-sulfur; 4Fe-45.
NETAL 359 359 IRON-SULFUR (4FE-45)
NETAL 420 420 IRON-SULFUR (4FE-45)
                                                                                                                                                                                                                                                                                            STRAIN-972;
MEDLINE-21848401; PubMed-11859360;
Wood V., GWilliam R., Rajandraam M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 199262; CAB16402.1; -...
InterPro; IPR000573; Aconitase_C.
InterPro; IPR001030; Aconitase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000511; Aconitase_N; 1.
FIGREAMs; TIGR00170; leuc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00450; ACONITASE_1;
PS01244; ACONITASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004431; Leub.
Pfam; PF00330; aconitase; 1
Pfam; PF00694; Aconitase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0415; ACONITASE.
                                                                                                                                                                                                         Schizosaccharomyces.
NCBI_TaxiD-4896;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGREAMS; T
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                                                                                                            SPACSES.03
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                                                                                                                                                                                                                                                                                                                                                  574 IGORAFYEIRYDAD--GKEIP-DFVLNREPY-----RHATVLVAHDNEGC----- 615
| METAL: | 423 | 423 | IRON-SULFUR; (4FE-45) | BY SIMILARITY). | | | | | | | | |
| SEQUENCE | 758 AA; | 92782 MW; | CE78C36818380E47 | CRC64; |
| Query Match | 6.0%; | Score 91.5 | DB 1; | Length 758; |
| Best Local Similarity | 24.6%; | Precie | 100.70.98; | | | | | | | | | |
| Matches: | 51; | Conservative | 22; | Mismatches: | 85; | Indels | 49; | Gaps
                                                                                                                                                                                                                                                                                                       124 MESOPFIAMKFETDYFVKVVPFPSIKNESNYHPFFPRTRACDLILOPDNIACKPFWKPRN 183
                                                                                                                                           10 AAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHV-----IADAQNITIS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94131966; PubMed-8300539; BECK. R.G.P.M. Brick. R.G.P.M. Prinkman E., van Boxtel R., Bekkers A.C.A.P., Verhelj H.M., Tommassen J.; Molecular characterization of enterobacterial pldA genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane phospholipase A.*;
J. Bacteriol. 176:861-870(1994).
I- FUNCTION: HTDROLISIS OF PHOSPHATIDICHOLINE WITH PHOSPHOLIPASE A.2 (EC 3.1.1.4) AND PHOSPHOLIPASE A.1 (EC 3.1.1.4) AND PHOSPHOLIPASE A.1 (EC 3.1.1.3) ACTIVITIES.
I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                             526 -----VAGSV--SSGSAGIPKETVVEGIAAPLPMANVDTDKII---PKQFLKTIKRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
Phospholipase Al precursor (EC.3.1.1.32) (Detergent-resistant phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-acylhydrolase) (Outer membrane phospholipase A) (OM PLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolage; Lipid degradation; Outer membrane; Signal; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                        184 INISQHGSDMQVSFDHAP---HNFGFR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                   616 -----GS----SREHAPWALNDFGIR 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHPHLIPASEA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X76902; CAA54224.1; -.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02253; PLA1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C36971; C36971.
PIR; S40130; S40130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCBI_TaxID-585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA1_PROVU
P37447;
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PA1_PROVU
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Blochim, Blophys. Acta 994:191-193(1989).

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6 SDLNKKAI---ESYNWSDNANKDEVKFOLSLAFPLWR-GILGDNSLLGASYTORSWWOLS 121
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MEDLINE-88041034; PubMed-3478675;
MEDLINE-88041034; PubMed-3478675;
Minohara T., Dietzschold B., Craft C.M., Wistow G., Early J.J.,
Donoso L.A., Horvitz.J., Tao R.;
*Primary and secondary structure of bovine retinal.S antigen (48-kDa protein).*;
                                                                                                                                                                                                                                                                                                                                               6 GWILAMAALPEFACAQEATIDKVHDTPAVRGSIIANALQEHDNPFTLYPYESNYLLYTYT 65
                                                                                                                                                                                                                                         45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          47; NPVGKHVIADAQNITISQYACHDQVAVTI-----LWSPGALGIEFLKGFRVILE---ELK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splice variant of arrestin. Molecular cloning and localization in
                                                                                                                                                                                                                                                                                                          .. 5 GWRMKAAARPRICVANEGV-----GPASRNSGLYNITFRYDN-------CTTYL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wistow G.J., Katial A., Craft C.M., Shinohara T.; Sequence analysis of bovine retinal S-antigen. Relationships with alpha-transducin and G-proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89088273; PubMed-2910351;
Tsunasawa S., Shichl H.;
"The amino acid sequence of S-antigen: N-terminus and uveitogenic
peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87156714; PubMed-2950857;
Manaki K., Takahashi Y., Sakuragi S., Matsubara K.;
*Molecular cloning of the S-antigen cDNA from bovine retina.";
Blochen. Blopples. Res. Commun. 141:904-910(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94253112; PubMed-7515057;
Smith W.C., Milam A.H., Dugger D., Arendt A., Hargrave P.A.,
Palczewski K.;
                                                                                                                                                                      DB 1; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
S-arrestin (Retinal S-antigen) (48 kDa protein) (S-AG) (Rod
                                                                                                                                                                                                                                         58; Indels
                              CHAIN 21 289 PHOSPHOLIPASE A1.
ACT_SITE 164 164 BY SIMILARITY.
SEQUENCE 289 AA; 32944 MW; D75516CFF8406997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 SEGROCOCLILKOPKOLNSSFKRTGMESOPFLAMKFETDYFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 84:6975-6979(1987).
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                                                                                                                                                   Query Match 5.6%; Score 85.5; Disbest Local Similarity 26.5%; Pred. No. 1.1; Matches 43; Conservative 16; Mismatches
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bovine retina.";
J. Biol. Chem. 269:15407-15410(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-12 AND 198-229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEBS Lett. 196:23-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    photoreceptor arrestin).
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                                                                                                                                                                                                                                                                                           MEDLINE-98154736; PubMed-9495348; "
Refaratin Jr., Wilden Jr., Choe H.W., Labahn J., Krafft B., Buldt G.; "
"X-ray crystal structure of arrestin from bovine rod outer segments.";
Nature 391:918-921(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1-FUNCTION: ARRESTINISONE OF THE MAJOR. PROTEINS OF THE ROS
-(RETINAL ROD OUTER SEGRENTS); IT BINDS TO PHOTOACTIVATED-
PHOSPHORYLATED RHODDOPSIN. THEREBE APPARENTLY PREVENTING THE
TRANSDUCIN-MEDIATED ACTIVATION OF PHOSPHODIESTREASE.
-1-ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM (P44); ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT
FORM PLAYS A ROLE IN THE PHOTOTRANSDUCTION CASCADE.
-1-TISSUE SPECIFICITY: RETINA AND PINRAL GLAND. THE P44 ISOFORM IS
LOCALIZED IN THE PHOTORECEPTOR OUTER SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEGATOR PROBLEM.

PROBATES PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

WEDLINE-9235986; Pubmed-10319246;
Hisch-G.A., Gebubert C., Gurevich V.V., Sigler P.B.;

"The 2.8 A crystal structure of visual arrestin: a model for
                                                                              MEDEINE-9026449; PubMed-2160981;
Ruppertz B., Weyand I., Bauer P.J.;
"Ca2-7-3inding rapacity of cytoplasmic proteins from rod
photoreceptors is mainly due to arrestin.";
J. Biol., Chem. 265:9470-9475(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26B1D80B652AF1EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F -> A (IN SHORT ISOFORM)
MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- DISEASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.
-1- MISCELLANBOUS: ARRESTIN BINDS CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
                                                                                                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ^
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPRO00698; Arrestin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrestin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J02955; AAA30378.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arrestin's regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97:257-269(1999)
                                                          CALCIUM-BINDING DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
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DB 1; Length 404;

85.5; DB No. 1.6;

5.6%; Score 20.6%; Pred.

Similarity

Local

Match

Query Best

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InterPro; IPR Pfam; PF00047

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Query Match 5.6%; Score 85; DB 1; Length 429;
Best Local Similarity (18.6%; Pred. No. 2; J. 18.6%; Antches 52; «Conservative" 42; Mismatches 92; Indels 94; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between "the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 TTSITSILPVDAKDWIEGEGYQCRVDHPHPPRPIVRSITKAPGKKSAPEVYVFLPPEEEE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                             209 ITTLIPPSPLDLTENGTPRLTCLVLDLESEENITVTWVRERKKSIGSASQRSTKH--HNA 266
                                                                                                                                                                                                                                                     160 GKLASTYSKLNITQQQWMS---ESTFICKVI-----SQGENIWAHIRRCSDDEPRGY 208
                                                                                                                                                                                                                                56. DAQNITISQIAC --- HDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDP 112
                                                                                                                                                                                                                                                                                                    113 KOLNSSFKRIGMESOPFLNMKFETDFFVKVVPFPSIKNESNYHPFFFRTRACD-----
                                                                                                                                                                                                                                                                                                                                                                         .166 -- LLLQPDNLACKPEWKPR-----NLNIS-----QHGSDMQVSFDHAPHN-
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3, Last sequence update)
), Last annotation update)
S-antigen) (48 kDa protein) (S-AG) (Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- DISBASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.
-I- MISCELLANBOUS: ARRESTIN BINDS CALCIUM (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
                                                                                 168 R'-> N (IN REF. 2).
308 P -> L (IN REF. 2).
48671 MM; D2970B34EF8A72B0 CRC64;
                     Fr. De. J. C. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Netazoa, Chordata, Cranlata, Vertebrat<u>a,</u>
Mammalia, Eutheria, Cetartiodactyla, Suina, Suldae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 OTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDKRTLTCLIONFFPEDISVOWLODSKLIPKSOHSTTPL 366
                                                PROSITE: PS00290; IG_MHC; 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
16-CT-2001 (Rel. 40, Last ann
5-arrestin (Retinal S-antigen)
SWART; SW00410; IG_11ke; 3. SWART; SW00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   photoreceptor arrestin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBL_TaxID-9823;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit. Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 PGALGIEFLKGFRVILEEL-----KSEGRQCQQLILKDPKQLNSSFKRTGMESQPF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 LUMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACD--LLLQPDNLACKPFWK----- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 LVTRENDYYPIPNIHPPLSVNETREKPTYHHCTLLDGELVLENRNVS-EPVLRYVIFDAL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PRNL---- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AIHGKCIIDRPLPRRLGYITENVMKPFDNFKKHNPDI-VNSPEFPFKVGFKTMLTSYHAD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 DVLSKMDKLFHASDGLIYTCAETPYVFGTDQTLLKWKPAEENTVDFQLEFVFNEVQDPDL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sacco A.G.; "Cloning and characterization of zona pellucida genes and cDNAs from a variety of mammalian species: the ZPA, EPB and EPC gene families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 PGSQPVSFER--RHLEETLMQRDTFVCERTDGLRCLLFLINDPD-:----KGEGV----F 88
                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPRO01339; mRNA_cap_ensyme.
Pfam; PF01331; mRNA_cap_ensyme; 1.
Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris J.D., Hibler D.W., Fontenot G.K., Hsu R.T., Turewicz B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last anoctation update)
Lons pellucida sperm-binding protein 2 precursor (Zona pellucida 2Pycoprotein ZP2) (Zona pellucida protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 5.5%; Score 84; DB 1; Length 449; Best Local Similarity 20.4%; Pred. No. 2.6; Matches 56; Conservative 34; Mismatches 92; Indels 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- KLKHEGPFKRKTCKQEQTTETTSCLLQNVSPG-----DYIIELV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . GUANYLYLATION SITE (POTENTIAL)
                                                                                           -1- SUBCELIUTAR LOCATION: Nuclear:
-1- SIMILARITY: BELONGS TO THE EUKARYOFIC GTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 435 POLY-GLN.
449 AA; 52253 MW; D93F44BF112305BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDINTTRKVMHYALKP-----VHSPWA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::| || || || 267 DERDPTSTYLDYDAKPNLIKLRVWQGSNVHTDFA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 716 AA
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Okazaki Y., Isojima S., Sugimoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
MEDLINE=95143578; PubMed=7841460;
                                                                        AN RNA 5'-TRIPHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; D83180; BAA11833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a variety of mammallan sp
DNA Seq. 4:361-393(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2P2_FELCA
P47984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253
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                                                                                                                                                              InterPro: IPR000658; Arrestin.
Pfam; PF00339; Arrestin.1
Pfam; PF00339; Arrestin.2
ProDom; PR000309; Arrestin; I.
PROSSITE; PR00095; Arrestin; I.
PROSSITE; PR00035; Arrestin; I.
PROSSITE; PR00199; Arrestin; I.
PROSSITE; PR00199; Arrestin; I.
PROBABLE.
SEQUENCE 405 AA; 45102 MW; P90006658GEFA73E CRO64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of the mRNA-capping enzyme and ferric-reductase-related genes from Candida albicans.";
Microbiology 142:2515-2523(1996).

-i. FUNCTION: SECOND STEP OF M-RNA CAPPING. TRANSFER OF THE GNP HOIETY OF GTP TO THE 5'END OF RNA YIELDING A 52 KDa ENZYME-GMP COVALENT REACTION INTERMEDIATE.

-i. CATALITIC ACTIVITY: GTP + (5')PP-pur-mRNA = diphosphate + (6')PP-pur-mRNA = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G(5')PPP-PUT-MRNA.
SUBUNIT: THE M-RNA CAPPING ENZIME IS COMPOSED OF TWO SEPARATE
CHAINS ALPHA AND BETA, RESPECTIVELY A MRNA GUANTIZITRANSFERASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ETD-YFVKVVPFPSI------KNESNYHPFFFRTRACDLLLQPDNLACKPFW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 KPRNLNISQ-HGSDMQV----- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPAPODVGKCCGVDFEVKAFATDSADTGEDKIPKKSSVRLLIRKVQHAPLENGPQPHAEA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 -FRFFY----LHYKLK------HEGPFK---RKTCKQEQTTETTSCLLQNVS-----PG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75. ILWSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPKOLNSSFKRTGMESOPFLNMKF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 AWQFFWSDKPLHLTVSLSKELYYHGEPIPVTVTVTVTNTEKTVKKIKALVEQVANVVLYSS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 ANEGVGPASRNSGLYNITFRYDNCTTYLNPVGKHVIADAQNITISQYACH-DQVAV---T 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3, ANVOASKSTPNHVIERKTSRDKSVTIXL---GKR------DYIDHVDQVEPVDGV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 VLVDP-----ELVKGKRVIV--------SLTCAF-RIGGEDIDVIGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tamada-Okabe T., Shimmi O., Doi R., Mizumoto K., Arisawa M.,
Tamada-Okabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.5%; Score 84; DB 14 Length 405; Best Local Similarity 21.5%; Pred. No. 2.3; Matches 56; Conservative 31; Mismatches 97; Indels 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.NOV-1997 (Rel. 35, Last sequence update)
02.NAY-2000 (Rel. 39, Last annotation update)
mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)
(EC. 2.7.7.50) (GTP--RNA guanylyltransferase) (GTase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 AA.
                                                                     or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                      EMBL; 582664; AAB46757.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96425877; PubMed-8828219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 39, Last anno
                     . i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 |: | |: | 356 DYTERPVATERTOOKV 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYLIELVDDTNTTRKV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans (Yeast).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-5476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCE1_CANAL
P78587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
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13;

Gaps

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177. 25

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MEDLINE-92084094; PubMed-1684166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSFAC; T01970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox; DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (
01-NOV-1995 (
15-JUN-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; LIM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A39479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Katches
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                         between the Swiss Institute or Biguinghaman, where are no restrictions on its the European Bloinformenties Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Wusage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 VPFPSIKNESNYH----PFFFRTRACDILLQPDNLACK-PFWKPRNLNISQHGSDMQVS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VEFPSDFGTKKWHTSVVDPFSFELLNCTYILDPENLTLKAPYETCTRRTLGQHRMIIRLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 FDHAPHNFGFRFFTLHYKLKHEGPFKRKTCKQEQTTET-----TSCLLQ-----NVSP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 ---- DHNAASRHNSLAYQI------NCPVMQAEETHERAGSTICTKDSMSFTFNVIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID-31233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZONA PELLUCIDA SPERM-BINDING PROTEIN 2. EXTRACELLULAR (POTENTIAL).
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-1: FUNCTION: EP2 FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA, IN WHICH EP2 AND EP3. COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
                                                                            . . 1722 ACTS AS A SECONDARY SPERM RECEPTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: FS00683; IP_DOMAIN; 1.
31ycoprotein; Stgnia: Sulfation; Sperm; Receptor; Transmembrane;
Stracellular matria:
                                                                                                                         # mattix.
-1--PIM: SULFATED GLYCOPROFEIN WITH O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-1--SIMILARITY: CONTAINS 1 2P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 82; DB 1; Length 716; 24.5%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V -> G (IN REF. 2).
L -> P (IN REF. 2).
F -> S (IN REF. 2).
C5745496E82CB671 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 24.5%; Pred. No. 7.1;
hes 35; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           or send, an, email to licenseelsb_sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001507; Endoglin/CD105.
fam; PF00100; zona_pellucida; 1.
*RINTS; PR00023; EPELLOCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        245 GDYIIELVDOTNTTRKVMHXALK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 G----LADENTDIKNPMGWSIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mechanosensory protein 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716 AA;
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Way J.C., Wang L., Run J.Q., Wang A.,

"The mec-3 gene contains cis-acting elements mediating positive and negative-regulation in cells produced by asymmetric cell division in Caenorhabdits elegans."

Genes Dev. 5:2199-2211(1991).

Genes Dev. 5:2199-2211(1991).

TO STES IN THE MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH RECEPTOR NUTHONS. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86.

TO STEES IN THE MEC-3 GENE PROMOTER.

-1 SUMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.

-1 SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 NESNYHPFFFRTR-----ACDLLLQPDNLACKPFWRPRNLNISQHGSDMQVSFDHA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 PHNF----GFRPFILHTKLKHEGPFKRKTCKQEQTIETTSCLL--QNVSPGDYIIELVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 SHRCAGCKKGVSPTDMVTKLKAGLVFH------VECHCCSLCGRHLSPGEQI--LVD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 NEQIYDRFIYRADNHSYHENCVKCTICESP--LAEKCFWKNGRIYCSOH-----YYKDHS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.binding; Nuclear protein; Developmental protein;
domain; Metal-binding; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4%; Score 81.5; DB 1; Length 320; 31.1%; Pred. No. 2.9; (tive 9; Mismatches 47; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC).
AF98BD31C2B2FDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; FALSE_NEGPROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 320 A
320 AA, 36849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSFAC; TU19/0; -.
nterPro; IPR001356; Homeobox.
nterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roDom; PD000010; Homeobox; 1.
roDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X63956; CAA45377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fam; PF00046; homeobox; 1. fam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein HI1369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX;
SMART; SM00132; LIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 DINTIRKVM-HY 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                              Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocgyne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidmann J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 SOTACHDOVAVTILMSPGA-LGIEFLK --GFRVILEELKSEGROCOQLILKDPRQLN--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 RHCIGCEGINLEIENPQHEPSIELTORCNIACIY--CYSRLKTVRRGIRGNIEBAETVTI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RLCVANEGVG------PASRNSGLINITERIDNCTTYLNPVGKHV---IADAQNITI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Welinder K.G.;
se and cDNA
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MEDLINE-93238741; PubMed-8477731;
Baunsgaard L., Dalboege H., Houen G., Rasmussen E.M., Welinder Panins acid sequence of Coprinus macrorhizus peroxidase and CDNF sequence encoding Coprinus cinereus peroxidase. A new family of fungal peroxidases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 5.3%; Score 81; DB 1; Length 286; Best Local Similarity 28:2%; Pred: No. 2.8; Matches 46; Conservative 22; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 161-185.
MEDLINE-92247803; PubMed-1576150;
Kfalke M., Andersen M.B., Schneider P., Christensen B., Schuelein M., Welinder K.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR;: MJ0804; -. Pfam: PF01444; MoaA_NifB_PqqE; 1. Bypothetical protein; Complete proteome. SEQUENCE 286 Aa; 32920 MW; CACC47C3A3B4E63A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117, ----SFERRIGMESOPFLAMMRPETDYFVKVVPFPSIKNESNY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 IMISLSSFSR---EKYKLLTGK---DYFNRVL--NNIKIASKY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Agaricales; Psathyrellaceae; Coprinopsis.
NCBL_TaxID=5346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER_COPCI STANDARD; PRT; 363 AA. P28314; P28315; 01-DEC-1992 (Rel. 24, Created) 01-UL-1993 (Rel. 26, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Peroxidase precursor (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coprinus cinereus (Inky cap fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Blochem. 213:605-611(1993).
                STRAIN-JAL-1 / DSM 2661 / ATCC 430
MEDLINE-96337999; PubMed-8688087;
                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67525; AAB98804.1; -.
  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 QHQNFSSLK-SPYADELSLSFDQNMGNFALKLGYIHRDNKNRIILKREPIQGERRTSYIN 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 RVILEELKSEGROCOQLILKDPK-----QLNSSFKRTGMESQPFLNM-KFETDYF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 VKVVPFPSIKNE-----SNYHPF----SNYHPF-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 PFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTT---- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
STRAIN-Rd / KW20 / Adams N.D., White O. Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerney K., Sutton G., Fitzhugh W., Fidalds C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Relley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblow E., Cotton N.D., Weldman J.F., Phillips C.A., Spriggs T., Hedblow E., Cotton M.D., Weldman J.E., Nguyen D.T., Saudgk D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
  Racmophilus influenzae.
Bacteria: Proteobacteria: gamma subdivision: Pasteurellaceae;
Racmophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 5.4%; Score 81.5; DB 1; Length 839; I Similarity 18.2%; Pred. No. 9.7; 36; Conservative 42; Mismatches 69; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12× × 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bypothetical protein; Complete proteome,
SEQUENCE 839 AA; 96409 MW; D419EFF3BF91E503 CRC64;
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5-DEC-1998 (Rel. 37, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
70804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
-1- SIMILARITY: TO E.COLI YDDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000531; TonB_boxC. Pfam; PF00593; TonB_boxC; 1.
                                                                                        NCBI_TaxID=727;
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Best Loc Matches

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15-DEC-1998 16-OCT-2001 Y804_METJA 058214; 01-NOV-1997

650

RESULT 12 T 804 MED T 804 M AC 058214 M DT 01-NOV DT 15-DEC DT 15-DEC DT 16-OCT DE HYDROH GN MYDROH GN MYDROH OS Archae OC Archae OC Methan OC Methan OC Methan

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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY.

xidoreductase; Glycoprotein; Peroxidase; Heme; Calcium-binding; Pfam; PF00141; peroxidase; 1.
Rentwrs; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE.
2; 1. IPR002016; Peroxidase. EMBL; X69457; CAA49216.1; ... HSSP; P28313; 1ARV. aterPro;

N-LINKED (GLCNAC...) (HIGH MANNOSE). IRON (PROTOHEME IX AXIAL LIGAND).
PYRROLIDONE CARBOXYLIC ACID. (VIA CARBONYL OXYGEN). (VIA CARBONYL OXYGEN). DISTAL HISTIDINE. PEROXIDASE. DISULFID CARBOHYD CT_SITE ISULFID ISULFID I A BIND A BIND IOD RES ignal. 'A BIND A BIND A BIND A BIND A BIND TARIANT

----FRVILEELKSEGROCQQLI-----LKDP 112 Gaps 39; 5.3%; Score 80.5; DB 1; Length 363; 43; Indels Best Local Similarity 22.8%; Pred. No. 4.2; Matches 31; Conservative 23; Mismatches 79 PGALGIEFLKG----**Ouery Match** Š

37640 MW; E56EB53B963C3DB5 CRC64;

363 AA;

SEQUENCE

X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE-2400206; PubMed-9257700;
Itakura H., Oda Y., Fukuyama K.;
"Binding mode of benzhydroxamic acid to Arthromyces ramosus
peroxidase shown by X-ray crystallographic analysis of the complex at
1.6-A resolution.";
PEBS Lett. 412:107-110(1997). 149 PGSPRIEFITGRSNSSOPSPPSLIPGPGNTVTAILDRMGDAGFSPDEVVDLLAAHSLASQ 208 113 KOLNSSFKRTGMESOPFINMKFETDYFVKVV-----PPPSIKNESNYHPP--FFRTRAC 164 "Crystal structure of the fungal peroxidase from Arthromyces ramosus at 1.9-A resolution. Structural comparisons with the lighth and cytochrome c peroxidases.";
3. Mol. Biol. 235:331-344(1994). MEDLINE-92247803; PubMed-1576150; Kfalke M., Andersen M.B., Schneider P., Christensen B., Schuelein M., Welinder K.G.; "Comparison of structure and activities of peroxidases from Coprinus Cloning, sequencing, and heterologous expression of a gene coding X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE-94118276; Pubmed-8289254; Kubishima N., Fukuyama K., Matsubara H., Hatanaka H., Shibano Y., SEQUENCE FROM N.A. MEDLINE-9539997; PubMed-7670182; Saval-Hatanaka H., Ashikari T., Tanaka Y., Asada Y., Nakayama 1 Minakata H., Kunishima N., Fukuyama K., Yamada H., Shibano Y., Coprinus macrorhizus and Arthromyces ramosus."; Bukaryola; Fung1; Fung1 Incertae sed1s; 'Arthromyces'
NCBL_TaxiD-5451; -1- SUBCELLULAR LOCATION: Secreted. -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. losci. Biotechnol. Biochem. 59:1221-1228(1995). 01-OCT-1996 (Rel. 34, Last sequence update) 15-UUN-2002 (Rel.,41, Last annotation update) Peroxidase precursor (BC 1.11.1.7). Arthromyces ramcous. Blochim. Blophys. Acta 1120:248-256(1992). for Arthromyces ramosus peroxidase. 01-DEC-1992 (Rel. 24, Created) 266 ALLARDSRTACE -- WO 279 165 DLLLQPDNLACKPFWK 180 STANDARD; SEQUENCE OF 162-186. PER ARTRA Amachi T.; Machi T.; 유 윱 .8 8

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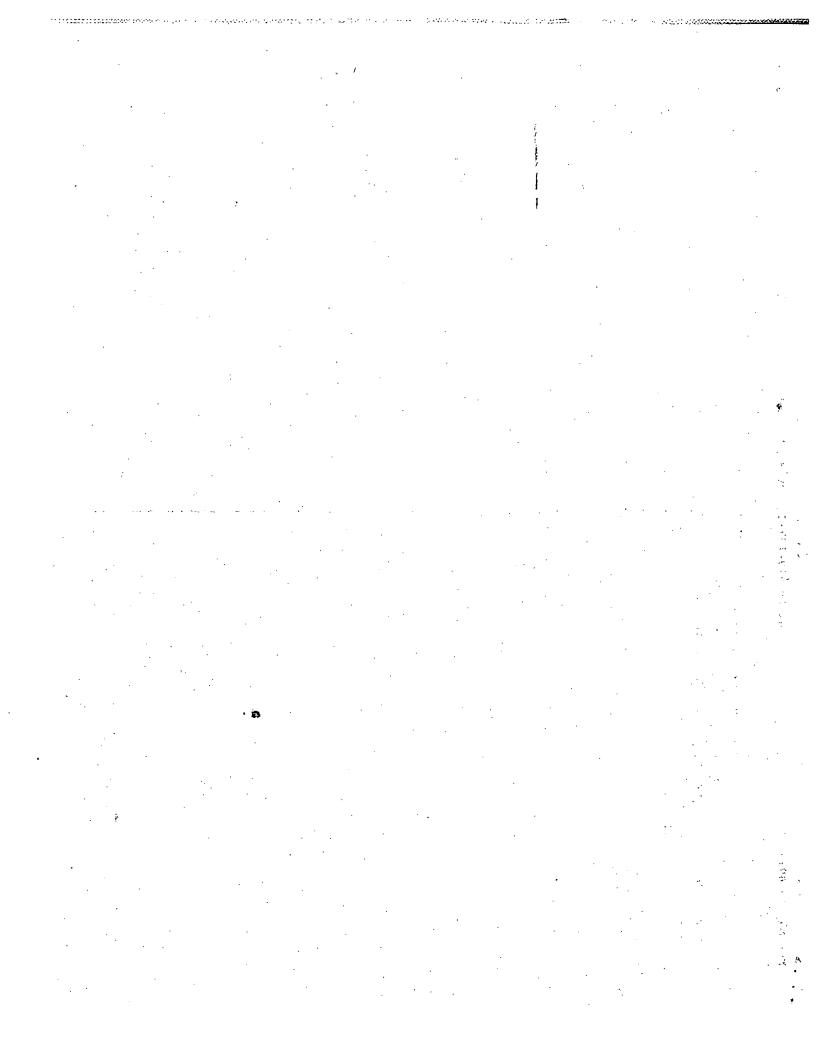
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        EMBL outstation
                        the European Bioinformatics institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Glycoprotein; Peroxidase; Iron; Heme; Calcium-binding; 3D:structure; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGALGIEFLKG------LKDP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 KOLNSSFRRIGMESOPFLANKFETDIFVKVV-----PPPSIKNESNYHPF--FFRIRAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VIA CARBONYL OXYGEN).
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(Rel. 35, Last sequence update)
                                                                                                entities requires a license agreement (Se or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEROXIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00435; PEROXIDASE_1; 1. PS00436; PEROXIDASE_2; 1.
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                                                                                                                                                                     BAA09861.1; -.
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ARRS_CANFA
ID ARRS_CANFA
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DT 01-NOV-1997 (;)
DT 01-NOV-1997 (;)
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between
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dekcomien G., Epplen J.T.;
Dekcomien G., Epplen J.T.;
20 dog breeds for gPRA.;
submitted (kov-2001) to the EMBL/GenBank/DDBJ databases.
10 dog breeds for gPRA.;
submitted (kov-2001) to the EMBL/GenBank/DDBJ databases.
11 FUNCTION: ARRESTIN IS ONE OF THE MAJOR PROTENTS OF THE ROS (RETINAL ROD OUTER SEGNENTS); IT BINDS, TO PHOTOACTIVATED-PHOSPHORYLATED REDOPEST. THERMS TO PHOTOACTIVATED.
11 TISSUE SPECIFICITY: RETINAL AND PINRAL GLAND.
11 TISSUE SPECIFICITY: RETINAL AND PINRAL GLAND.
11 DISEASE.S ANTIGEN INDUCES AUTOIMMUNE UVEITIS.
12 MISCELLANEOUS: ARRESTIN BINDS CALCION (BY SIMILARITY).
13 SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 IVIVDPBLVKGKKVYVSLICAP-RIGGEDIDVIGLSFRRDLFFSQVQVFPPVRAGAPTK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQ-HGSDMQV---- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edm; PF02752; allection response respon
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation of canine retinal arrestin cDNA and exclusion of three candidate genes for Swedish Briard retinal dystrophy."; Curr. Eye Res. 16:270-274(1997).
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                Weske A., Nafstroem K., Fluckh U., Sargan D.R., Nilsson S.E.G.,
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   41, Last annotation update)
al S-antigen) (48 kDa protein) (S-AG)
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Briard X Beagle; TISSUE-Retina;
MEDLINE-97243904; PubMed-9088745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAD19827.1; JOINED CAD19827.1; JOINED
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                                                                photoreceptor arrestin).
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                                                                                        SAG OR SAGI OR ARR. Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X98460; CAA67100
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107 LQESLMKKIGGNTYPPLLTFPDYLPCSVNLQPAPQDMGKCCGVDFEVKAFAR 158	-	159 DSTEDEEDKVPKKSSVRLLIRKVQHAPSKMGPQPRAEAAMQFFMSDKPLHLAVSLSKEIY 218	221 FKRKTCKOBOTTETTSCLLONVSPGDYIIELVDDYNTTRKV 261	219 FEGEPITVTVTVTNHTEKTVKKIKALVEQVANVVLISSDITTKVAQEETQEKV 272
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Search completed: May 19, 2003, 09:20:48 Job time : 10.6447 secs



17 88 5.8 451 13 073719 073719 073719 035we8 931lus gall 18 88 5.8 173 10 05LRR0 095we8 931lus gall 095we8 5.7 12 12 12 089248 095we8 095we8	PRELIMINARY; PRT; 745 AA. O2 (TrEMBLrel. 21, Created) O2 (TrEMBLrel. 21, Last sequence update) O3 (TrEMBLrel. 21, Last sequence update) O3 (TrEMBLrel. 21, Last sequence update) O4 (TrEMBLrel. 21, Last sequence update) O5 (TrEMBLrel. 21, Last sequence update) O6 (TrEMBLrel. 21, Last sequence update) O7 (TrEMBLrel. 21, Last sequence update) O7 (TrEMBLrel. 21, Last sequence update) O6 (TrEMBLrel. 21, Last sequence update) O6 (TrEMBLrel. 21, Last sequence update) O6 (TrEMBLrel. 21, Last sequence update) O7 (TrEMBLrel. 21, Last	Query Match 52.0%; Score 788; DB 13; Length 745; Best Local Similarity 53.8%; Pred. No. 4.3e-71; Matches 142; Conservative 40; Mismatches 80; Indels 2; Gaps 1; QY 17 CVANEGVGPASRNSGLYNITEKIDNCTYLAPVGKHVIADAQNITISQTACHDQVAVT 74
Gencore version 5.1.4_p5_4578 Copyright (c) 1993 2003 Compugen Ltd. OM protein - protein Search, using sw model Run on: May 19, 2003, 09:14:29; Search time 21.809 Seconds (without alignments) 2626.495 Million cell updates/sec Title: US-09-912-157-2_COPY_36_313 Sequence: 1 ANTCGMPMKAAARPRICVAN Scoring table: Gapop 10.0, Gapext 0.5 Searched: 671580 seqs, 206047115 residues Total number of hits satisfying chosen parameters: 671580 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100* Listing first 45 summaries	Database: SFTREMEL_21:* 1: Sp_Archea:* 2: sp_Dacteria:* 4: sp_Langi:* 5: sp_Lanman:* 6: sp_nammal:* 7: sp_namial:* 10: sp_panial:* 10: sp_panial:* 11: sp_rodent:* 11: sp_rodent:* 12: sp_rive:* 13: sp_rive:* 13: sp_rive:* 14: sp_unclassified:* 15: sp_Langi:* 15: sp_Langi:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_bacteriap:* 19: sp_bacteriap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_bacteriap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_bacteriap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_bacteriap:* 16: sp_bacteriap:* 17: sp_archeap:* 18: sp_bacteriap:* 18: sp_bacteriap:* 19: sp_archeap:* 10: sp_bacteriap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_bacteriap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 1	1 788 52.0 745 13 Q8QHJ9 Q8qhJ9 brachydanlo 2 779 51.4 745 13 Q8RHJ6 G8GHJ6 Drachydanlo 4 695 564 4 Q9DFA0 Q8R5J6 Q8R5J6 Q8R5J6 Q8R5J6 Q8R5J6 Q8R5J6 Q8R5J6 Q9L6A0 Q9L6A0

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. 61 SEDANDURGERGEHULTKIKKHEGPFRRTCRODONTETTSCLLONVSPGDYILELVDDS 120
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                                                                                                                                                                                                                                                                                                                                                136 IDYFVKVVPFPSIKNESNYHPFFFRTRACDLILQPDNLACKPFWKPRNLNISQHGSDMQV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 HPFFFRTRACDLLLOPDNLACKPFWRPRNLNISOHGSDMQVSFDHAPHNFGFRFFYLHYK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKHEGPFRRICKOROTTETTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IDYEVKIVPEPSIKNESNYHPFFFRTRACDLLLQPDNIACKPEWKPRNLNISQHGSDHHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBL_TaxID-10090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TESTIS;
Bloecker H., Boecher M., Brandt P., Mewes H.W., Gassenhüber J.,
                                                                                               MEDLINE-21824237; Pubmed-11802165;
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/NAPR-mediated FGF
                                                                                                                                                                                                                                                                        Ouery Match (5.9%; Score 695; DB 11); Length 582; Bestilocal Similarity 86.0%; Pred. No. 8.5e-62; Matches 123; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 691; DB 4; Length 564; 99.2%; Pred. No. 2.1e-61; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;
                                                                                                                                                                                                                                      582 AA; 65263 MW; 56663B2981C4268E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGUFAO PRELIMINARY; PRT; 564 AA.
09UFAO;
01-MAX-2000 (TIEMBLEA: 13, LAST sequence update)
01-MAX-2000 (TIEMBLEA: 13, LAST sequence update)
01-MAX-2000 (TIEMBLEA: 13, LAST annotation update)
Bypothetical 63.1 kDa protein (Fragment).
                                                                                                                                                         signalling."; //
Nat. Cell Biol. 4:170-174(2002).
EMBL; AF424804; AAL79530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 NITRKVMHYALKPVHSPWAGPIR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.2
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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09ZE66
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                     SP DR FF FF SP SO
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                   195 VSFDHAPHNFGFRFFYLHYKLKHEGPFKRRTCKQEQTTETTSCLLQNVSPGDYLIELVDD 254
                                          75 ILWSPGALGIEFLKGFRVILEELKSEGROCQQLILKDPRQLNSSFKRTGNESQPFLNNKF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ETDYFVKVVPFPSIKNESNYHPFFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 CVANEGVGPASRNSGL--TNITFRYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Ebiaryotei Metaroa: Chordata; Craniata; Vertebrata; Enteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21824237; PubMed-11802165;
Furthauer M., Lin.W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuerthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AR401323; AAL78817.1; SEQUENCE 745 AA; 83437 MW; 75BB9EDCC08A4652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80; Indels
                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLRel. 21, Created)
01-JUN-2002 (TrEMBLRel. 21, Last sequence update)
01-JUN-2002 (TrEMBLRel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R5J8 PRELIMINARY, PRT; 582 AA. Q8R5J9; 01-500-2002 (TERBLEI 21, Created) 01-JUN-2002 (TERBLEI 21, Last sequence update) 01-JUN-2002 (TERBLEI 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.4%; Score 779; DB 13;
53.0%; Pred. No. 3.5e-70;
1ve 42; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Last annotation u Similar expression to FGF protein (Fragment).
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                                                                                                                                                                                                                                    PRT; 745 AA.
                                                                                           255 THTTRKVMHYALKPVHSPWAGPIR 278
                                                                                                              275 SINTEROTOTHYSQVHSPWAGPIR 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ignalling.";
at. Cell Biol. 4:170-174(2002).
                                                                                                                                                                                                                                                                                                                                 FGF signaling antagonist Sef.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 53.08 Matches 140; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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080HJ6
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1D 08R5
1D 08R5
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128 PFINNKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNIACKPFWKPRNLNIS 187
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                                                                                                                                                                                                                                                       423 RELAKINCIQCRKVQRKRPQKGLLIQLQDMVCQPNSTDYTGPRQVLKGTCKIGMVDYRHCE 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 QHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | : | | : | 22
                                                                                                                                                                                                                -------DPRQLNSSFKRTGM----ESQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GRQCQQLILKDPKQLNSSFKR---TGMESQPF------LNM---KFETDIFVKVV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enkaryota; Metazoa; Mematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis
MCBI_PaxID-6239;
                                                                                                                         77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 93; DB 5; Length 662;
23.4%; Pred. No. 1.2;
rative 24; Mismatches 65; Indels 78;
                                                    6.3%; Score 95.5; DB 12; Length 1341; 1.6%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                  Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
Scheet P., Maggi L., Dubbelde C.;
The sequence of C. elegans cosmid C39F7.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL.AF101310, AAC69214.2;
InterPro; IPR000310; BTB.POZ.
InterPro; IPR000345; CytC_heme_bind.
SNART; SN00225; BTB; 1.
PROSITE; PS001990; CYTCCHROME_C; UNKNOWN_1.
BTPOCCHE all protein.
SEQUENCE 662 AA; 75799 MW; DD64BBCA0579E102 CRC64;
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01-OCT-2001 (TrEWBLrel. 18, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
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556 KICSGDNTFCSKFACHNELPEVHCEVAPGAGPI 588
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                  25;
                                                                                                                                                                                                            95 EELKSEGROCOOLILK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical 75.8 kDa protein. C39F7.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 23.4% Matches 51; Conservative
                                                                                  Local Similarity 21.6
Les 46, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 NHGGKVSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UAQ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 RLKVTVIGAGDEKTNVNRGIWISGLYGVNKQGVWKNIPKYQGRTT----GLTIGADAEF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 KSEGROCOQLILKDPKQLNSSF-KRTGMESQPPLNMKFETDYFVKVVPFPSIKNE----S 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 TSYG---HNYIKNKSKNLNKIIGKYQNNNFQTILINYKYRTKYNLHFIPSIGFKYDYSRAS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 NYHPFFRATRACDILLQPDN------LACKPFWKPRN--LNISQHGSDMQVSFDH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 NYKE--YNVDIENLMIQKKSNOSFESSIGAKIVSKPIISKNNIILTLSAHG----- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 APHNFGFRFFYLHYKLKHEGPFRRKTCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTR 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.5%; Score 99; DB 16; Length 341;
Best Local Similarity 22.1%; Pred. No. 0.12;
Matches 69; Consexyative 35; Mismatches 120; Indels 88; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 INNHDVIGIAYSNLESKIKYNKKLGKTAVHGHLL-----SVYGLKELVKGFS--LQSI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 RLCVANEGVGPASRN-----SGLYNITF-----KTDNCTTYLNPVGKHVIADAQ- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 -------NITISQYACHDQVAVTILMSPGALGI-EFLKGFRVILEEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Pouter T., Alsmark U.C., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G., The genome sequence of Rickettsla prowazekil and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-ROY-1996 (TERBLACH. 01, Created)
01-ROY-1996 (TERBLACH. 01, Last sequence update)
01-BOZ-2001 (TERBLACH. 19, Last annotation update)
61-POZ-2001 (TERBLACH. 19, Last annotation update)
61-POZ-2001 (TERBLACH. 19)
61-POZ-2001 (TERBLACH. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glass P.J., Parker H.D.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U30500; AAA75043.1; -.
SEQUENCE 1341 AA; 148766 WW; DDCE6BEDEC4F9B68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 AA; 38808 MW; A43DAC317CBA42DB CRC64;
                                                                 Ol-MAY-1999 (Tribulical, 10, Created)
Ol-MAY-1999 (Tribulical, 10, Last sequence update)
Ol-MAY-1999 (Tribulical, 19, Last amoutation update)
190 (May antigen precursor (SCA))
                 341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 396:133-140(1998).
EMBL; AJ235270; CAA14551.1;
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MADRID E; WEDŽINE-9903993;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                 ckettsia prowazekil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 ETNYTHKKYHS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 KVMHYALKPVHS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID-782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, SEQUENCE 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-28292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondria.
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Drosophilidae, Drosophila.
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                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam:
               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          84 EF - F F - F F - F - F - F - F - GRICONSRRPINSFLRDFESGRIVSGRINILERFTSIRANRAF 128
                                 107 - SQHGSDMQVS--FDHAPHNF-----GFRFFTLHYKLKHEGPFKRKTCKQEQ 230
                                             129 VSORCINIAISANYDENPENCECKORELKFERDDAVEIFLKSYIXHBQWPENLGSERLEG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 NYHPFFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFY-- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ILEELKSEGROCOOLILKDPROLNSSFRRTGMESOPFLNMKFETDYFVRVVPFPSIKNES 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 ......EGPFKRKTCKQEQTTETTSCLLQNV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 FDAKTALKDMOGELLDGHSLELKISHRENADKGAIKRKEVKOKBOGECTKLLVRNL 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.1%; Score 93; DB 5; Length 872;
Best Local Similarity 22.7%; Pred. No. 1.6;
Matches 40; Conservative 27; Mismatches 63; Indels 46;
                                                                                                                                                                                                                                                                                            ubmitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           one;
Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50102; RRM; 5.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.
SEQUENCE 872 AA; 98043 MW; 65C86BFAESFE093E CRC64;
                                                                                                                                                                    01-NOV-1999 (TrEMBirel. 12, Created)
01-NOV-1999 (TrEMBirel. 12, Last sequence update)
01-MOV-2002 (TrEMBirel. 21, Last annotation update)
723F6.4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAX-2000 (TIEMBLEE]. 13, Last sequence update)
01-MAX-2002 (TIEMBLEE]. 20, Last annotation update)
                                                                      189) ICTDFGCFKKLEEDVKHMTKQDLKHGDLIIEVVDGKMT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 6
SWART; SW00360; RRM; 6.
                                                                                                                                                                                                                                                                                                                                                          investigating blology.";
Science 282:2018(1998).
EMBL; 283127;.CAB05631.1;
HSSP; P19339; 2SXL.
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                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTP69D protein.
PTP69D OR CG10975.
                                                                                                                                                                                                                                                                                    Oyd C.R.
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                                                                                                                         RESULT 8
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RA . Madaus M.D. Celniker S.E., IL P.W., Fvans C.A., Gocayne J.D.,
RA . Amanatides P.G., Scherer S.E., IL P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., IL P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,
RA . George R.A., Fortann J.R., Tandell W.D., Ihang Q., Chen L.X.,
Burdon R.C., Rogers T.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA . Maril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA . Beeson K.Y., Basud B. C., Helt G., Relson C.R., Miklos G.L.G.,
RA . Beeson K.Y., Basud M.R., Burnen B.P.; Bhandari D., Bolshakov S.,
R. Borkova D., Botchan M.R., Bouch J., Edstet B., Bolshakov S.,
R. Burtis R.C., Busam D.A., Dalike C., Davenport L.B., Davies P.,
RA . Burtis R.C., Busam D.A., Dalike C., Davenport L.B., Davies P.,
RA . Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Bothos B., Delcher A., Denike C., Perraz C., Ferriar S., Dunkov B.C., Dunn P.,
R. Bothos B., Delcher A., Garg N.S., Gelbart M.N., Glasser K.,
Glodek A., Gong F. Gorrell J.H., Garl W. H. W. Glasser K.,
A diodek A., Gong F. Gorrell J.H., Wel M.-H., Ibegvam C.,
Jalail M., Kalush F., Karpen G.H., Wel M.-H., Ibegvam C.,
Jalail M., Kalush F., Karpen G.H., Well M.-H., Ibegvam C.,
Jalail M., Kalush F., Karpen G.H., Well M.-H., Ibegvam C.,
Jalail M., Morfinch T.J., Mernades D.M., Welherefi A.,
Rumut S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Reinert K., Palano G.B., Pan S., Pollard J., Welberder F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Santh T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Santh T.,
R. Heng L... Raber B.C., Simpson M., Skupski M.P., Smith H.O.,
R. Heng E., Raber C., Weller E., Wen G., Shen B.,
R. Heng E., Raber C., Runner G., Wu D., Yang G., Khon G.,
R. Heng E., Raber C., Runner G., Wu D., Yang G., Khon G.,
R. Wang E., Raber C., Runner G., Wu D., Yang G., Khon G.,
R. Wang E., Raber C., Runner G., Runner B., Runner R., Runner R., Runner R., Runner R., Runner R., Runner R., Runner R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 92; DB 5; Length 1428;
20.8%; Pred, No. 3.9;
:Ive 40; Mismatches 104; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NCTTYLNPVGKHVIADA 57
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BQUENCE: 1428 AA; 163451 MW; 02B9C9FF94B706AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00383; TYR_PHOSPHATASE_1; 2, PROSITE; PS50056; TYR_PHOSPHATASE_2; 2. PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 NEGVGPASR-----NSGLYNITEKYD-----
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IPR003598; IG_C2.
IPR003609; IG_L1ke.
IPR00366; IG_MHC.
IPR000387; TX_Phosphatase.
IRR000242; Tyr_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00047; 1g; 2.
PF00102; Y_phosphatase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lyBase; FBgn0014007; Ptp69D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003540; AAF49892.1;
HSSP; P18052; IYFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69; Conservative
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223 TQLKIENNP-----PAKGFRG-----SDDWELH---RWSRMQSKEY- 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 VAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFRRTGMESQPFL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 NMKFETDYFVKVVPFPSIKNE--SNYHPFFFRTR-------ACDLL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 LOPDNIACRPFWRPRNIAISOHGSDMOVSFDHAPHNFGFRFFTLHTKLKHEGPFRRKTCK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 -- PSSSATISL--PHESGTITHCTRRKYSEEPAEHS--TKRPYMDTSPSEEDPFTRSGTP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosaugia; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 RPRICV -- ANEGVGPASRNSGLYNITEKYDNCTTYLNPVGKHVIADAQNITISQTACHDQ 70
                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 90.5; DB 13; Length 519; Best Local Similarity 20.9%; Pred. No. 1.5; Matches 61; Conservative 42; Mismatches 90; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 Q--EQTTETTS------CLLQNVSPGDXIIELVDD--TNTTRKVMHYA 265
                                             299 -----PGSTKTVRAQIIEQCTASPSCTHFGSSPGHYNSPGRIMELLE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01283; TB0X_1; 1.
PROSITE; PS01264; TB0X_2; 1.
PROSITE; PSS0125; TB0X_3; 1.
SEQUENCE 519 AA, 58080 MW; BB5E096C67PC3D1E CRC64;
                                                                                                                                                                                                   09W7C2
09W7C2
01-NOV-1999 (TEMBLIA: 12, Created)
01-NOV-1999 (TEMBLIA: 12, Last sequence update)
01-NAR-2002 (TEMBLIA: 20, Last annotation update)
T-box transcription factor Tbx5
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01-MAY-2000 (TrEMBIrel. 13, Last sequence update)
01-DEC-2001 (TrEMBIrel. 19, Last annotation update)
TVDS3.
                                                                                                                                                                                      519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horb.M.E. P. Thomsen G.H.;
ThyE. 18, essential for heart development.";
Development 126:1739-1751(1999).
EMBL, AF133036; AAD23592.1;
                                                                                                                                                                                         PRT;
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InterPro; IPR001699; TF_T-box.
Pfam; PF00907; T-box; I
PRINTS; PR00937; TBOX.
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-8355;
                                                                                                                                                                                09W7C2
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Q9PW79
                                                                                                                                   RESULT 11
359 NDGNDPIOKFFITLQEAGTPFFTHKDFINGSHTSYILDHFKPNTTFLKIVGKNSIGNG 318
                                                                                                 319 OPTOTATEST -- PRIFIP TO STANSTAUGHAND PRODUITION STANSTAUSE - 374
                                                                                                                                                                                                                                                                                                                             (409 - PRVRACEDLIK----TGGP-WSENVNGTIMDGVAIKPINISIQCHIDNYIRGNSIAINM 462
                                                                                                                                                                                                                                                                                                                                                                                          198 DHAPHNEGERFFYLHYKLKHEGPFKRKTC-----KOMPTETTSCLLONVSPGDYII 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                463 D-VPKTPNGKTLY ----ESVSPNTNYTVTVSAITRHKKNGEPATGSCLMPVSTPDAIGR 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99, KSBGRQCQQLILKDPKQLNSSFKRTGMESQPPLNMKFETDTFVKVVPFPSIKNESNIHPF 157
                                                                                                                                                                                                            375,5756.....FVPKVIEBAIXOONSRNLPIN-----FPDKLKTATDIE-- 408
                                                                                                                                                                                                                                                                                        158 PERTRACDILLQPDNLACKPFW-----KPRNLNISQH-----GSDMQVSF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 VVNDGFGPALPCGGALPERDVXD-----TDQYMLALIYHARWRRYECLTGDAAADA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWSPGALGIBFLKGFRVILEELKSE------GROCOQLILKDPKQLNS------ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 PVWDFYRGGDDGWGNALLFYPAIRNTTVLTVEANPWRGIDFG-----VPFP----SH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 6.0%; Score 91; DB 10; Length 506;
1. Similarity 20.8%; Pred. No. 1.3;
60; Conservative 34; Mismatches 82; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 THPFFFRTRACDLLLQPDNIACKPFWKPRNIAISQHGSDMQVSFDHAPHNFGFRFFYLHY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYAC--HDQVAVTI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECURENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan G., Ouyang S., Moffat K.S., Hill J.N., Gansberger Buener M., Burges S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Lismann V., Blunt S., Pai G., Vanaken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bypothetical So; kNa protein.
07yza sativa (Rice)
07yza sativa (Rice)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Richartoideae; Orygae. Oryga.
                                                   58 -----QNITISQYACHDQV_____AVIILMSPGALG-IEFLKGFRVILEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC034258; AAK54291.1; -.
Interpro; IPR004263; Exostosin.
Pfam; PP03016; Exostosin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 KLKHEGPFKRKTCKQ---EQTTETTSCLLQNVSPGDY----IIELVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56612 MW; B35878DIFICE24CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ELVDDINTTRKVMHYALK --- PVHSPWAGPI. 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 THWSKVNLDSK---YVLKLYLPKISERNGPI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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094LT2;
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Matches
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; DB 13; Length 368; 1.2;

49; Indels

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449 SSNQSEAISSALAARWGPYGAPAPEAGSTVSPFIGGFELQAHYLANEPDRALDLLRLQWG 508
                                                                                                                                                                                                                                                                                                                                                                                                                            248 RRTPDPRVETQRKLVPVLGENPIALLHRSFNTFVDYVPFPEWRRFG------RALDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 TAASKIKAAANARIADA------ONSLYR-----DNETTIHPODGNAWAIKANLTL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 SQYACHD-QVAVTILWSP-----GALGIEFLKGFRVILEELKSEGRQCQQLI---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 R-----ACDLILQPDNLACKPEWKPRNLNISQHGSDMQVSFDHAPHNFGFRFFY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 --LKDPKOLNSSFRRTGMESOPFLNMKFETDYFVKVVPFPSIKNESNYH-----PFFFRT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 FMLDDPRNTNSTF----IBG-----ISTDGSLAYAPTRNTPRVSHAHGWSTGPTSALT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TCGWRMRAAARPRICVANEGVGPASRNSGLINITFRYDNCTTYLNPVGKHVIADAQNITI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manzanares P., van Den Broeck H.C., de Graaff L.H., Visser J.
"Purification and Characterization of Two Different alpha-L-
Rhamosdidases, RhaA and RhaB, from Aspergillus aculeatus.";
Appl. Environ. Microbiol.
ENSE,: AF284761; AAK16249.1;
                                                                 PROSITE; PSOU199 4FEAS FERREDOXIN; UNKNOHN_1.
PROSITE; PSOU199 4FEAS FERREDOXIN; UNKNOHN_1.
PROSITE; PSOU652; THYRE NOFR_1; UNKNOHN_1.
PROSITE; PSSU0652; THYRE NOFR_1; UNKNOHN_1.
SEQUENCE 368 AA, 41531 M#; 0553CE531DEB47C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosidase; Hydrolase; Signal.
SIGNAL 1 19 POTENTIAL.
SEQUENCE 660 AA; 71218 MW; A550A9F4D0E42984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 HYTAGLRLTGPAGSTWLFKP-----QPGNLTEVQAGFETQLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or-oun-zuol (TrEMBLrel: 17, Last sequence update)
01-MAR-2002 (TrEMBLrel: 20, Last annotation update)
Alpha-L-rhamnosidase A precursor (EC 3.2.1.40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 QENDLYLÆQHDRVSCEPFYQMLNTWLNQQGSKASVN 335
                                                                                                                                                                                                                  f Match
Local Similarity 22.9%; Fred No. 1.2;
ies 36; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 89.5; Di
22.4%; Pred. No. 2.6;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21218536; PubMed-11319105;
Pfam; PF00020; TNFR_C6; 2. SMART; SM00005; DEATH; 1. SMART; SMORT; SMORT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 LHYKLKHEGPFKRKT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus aculeatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBL_TaxID-5053;
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                           Best Loca
Matches
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Q9C1M9
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                                                                                                                        Brojatsch J., Naughton J., Rolls M.M., Zingler K., Young J.A., CAZI., a. Every. Every properties at cellular receptor for cytopathic avian leukosis sarcoma viruses and mediates apoptosis.", cell 87:845-855(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 WSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPROLNSSFKRTGMESOPFLNM---- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 RRIPDPKVETQRKLVPVLGENPIALLHRSFNTFVDYVPFPEWKRFG------RALDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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($)
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MEDLINE-20193796; PubMed-10729132;
MEDLINE-20193796; PubMed-10729132;
MEDLINE-20193796; PubMed-10729132;
MEDLINE-20193796; PubMed-10729132;
MIGHORITICATION and Characterization of a THFR-related Receptor for Subgroups B/D/E Avian Leukosis Viruses Reveals Cysteine Residues Required Specifically for Subgroup E Virus Entry.";
J. Virol. 74:5572-3578(2000).
EMBL; AF161713; AAF60221:1;
HSSP; 014763; AD0G.
                                                                                                                                                                                                                                                              Ouery Natch 5.9%; Score 89.5; DB 13; Length 368; Best Local Similarity 22.9%; Pred. No. 1.2; Matches; 36; Conservative 19; Mismatches 49; Indels 53;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 ----- LLLLQPDNLACKPFWKPRNLNISQHGSDMQVS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 QENDLYLAEQHDRVSCEPFYQMLNTWLNQQGSKASVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001450; 4Fe45_ferredoxin.
InterPro; IPR000488; Death.
InterPro; IPR001368; INFR.c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                  PubMed-8945512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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RESULT 15 09x9S1

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LUII D., MUNOZ R., LOPEZ R., García E.,

LUII D., MUNOZ R., LOPEZ R., García E.,

SIGUÍA GENE (TÉS) located outside the cap locus directs the

Cormation of Streptococcus pneumoniae type 37 capsular polysaccharide

LYPE 37 pneumococci are natural, genetically binary strains.;

T. Exp. Med. 19:2111999).
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acteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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; Pred. No. 2.1;
43; Mismatches 117; Indels
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Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 509 AA; 58888 MW; C6C38D2ACFAB0D8A CRC64;
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-DEC-2001 (TrEMBLrel. 19, Last annotation update)
yascoharide synthase.
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Best Local Similarity 23.1%;
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Human cytokine rec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Mouse interleukin-Murine IL-17R prot Murine interleukin Murine interleukin Murine interleukin Murine II-17R poly Murine Interleukin Murine II-17R poly Murine II-17R poly Human IL-17 recept

Human secreted pro Human secreted pro Human IL-17 recept

Human PRO polypept Human EST encoded

ALIGNMENTS

Human IL-17R (bCTL Human Interleukin-Murine interleukin

D ABB07626 standard: Protein: 753 AA.	. AA.
XX	
AC ABB07626;	
DT 20-MAY-2002 (first entry)	
XX DE Human cytokine receptor, Zcytor18 amino acid sequence.	:18 amino acid sequence.
-	Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
	pulmonary alveolar protelnosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy.	14.3; gene therapy.
OS Homo saptens.	
PN W0200208259-A2.	
PD 31-JAN-2002.	
PF 23-JUL-2001; 2001WO-US23253.	•
XX	
R 26-JUL-2000; 2000US-220747P.	
XX	
PA (ZYMO) ZYMOGENETICS INC.	
XX	•
PI Presnell SR, Kuestner RE, Gao 2;	
_	
DR N-PSDB; ABA95031, ABA95032.	
	New cytokine receptor polypeptide designated zcytor18, useful for
pr inhibiting cell proliferation associated with psociasis or tumor	socotated with populacio or timor

Human Interleukin Human Interleukin

Human Interleukin Human Interleukin

ABB07627 standard; Protein; 753 AA.

(first entry)

20-MAY-2002

ABB07627;

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The invention relates to an isolated cytokine receptor polypeptide dealgnated Ecytori8. The Ecytori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit excell proliferation associated with psorialsis or tumour growth. The encoding nucleic acids are useful for providing Ecytoria in vivo by gene therapy techniques. Ecytoria oligonacieotide probes are useful for in vivo diagnosis, and the Ecytoria probes and primers can be used to detect and localize Ecytoria gross aberrations. In compose are also useful for a cletching gross aberrations, is changed in which ecytoria gross aberrations is changed in which inkage-based testing of pulmonary alveolar proteinosis, familial pariodic fever and erythroleukemia. and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Ecytoria amino acid sequence. and modulating immune system by binding to endogenous zcytor18; DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE 540 121 RIGNESOPFLNMKFETDYFVKVVPFPSIKNESNYHPFFFRTRACDILLLQPDNLACKPFWK 180 PRNINISOHGSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPFRRKTCKQEQTTETTSCLLQ. 240 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300 301 RKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFL 360 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 480 100.0%; Score 3829; DB 23; Length.753; 100.0%; Pred. No. 0; Atlye 0; Mismatches 0; Indels 0; Gaps ODFCGCEVALDLWEDFSLCREGOREWVIORIHESOFIIVVCSRGMKYFVDKRNYKHRGGG 420 KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 600 SQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG 660 1 ADTCGWRMKAAARPRLCVANEGVGPASRNSGLYNITFKYDNCTTYLNPYGKHVIADAQNI 60 Claim 1; Page 2; 119pp; English Best Local Similarity 100.0 Matches 718; Conservative 753 AA; Sequence 456 181 361 **4**21 481 241

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The invention relates to an isolated cytokine receptor polypeptide designated Zcytori8. The Zcytori8 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with positasis or tumour growth. The encoding nucleic acids are useful for providing Zcytori8 in vivo by gene therapy techniques. Zcytori8 oligonucleotide probes are useful for invivo diagnosis, and the Zcytori8 probes and primers can be used to detect and localize Zcytori8 gross aberrations in chromosome. In which Ecytori8 gene resides: The Zcytori8 probes are maples. The probes are also useful for detecting gross aberrations in chromosome. In which Ecytori8 gene resides: The Zcytori8 polyuciectides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with holymorphisms of cytokine receptors: The present sequence represents a human Zcytori8 variant amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor
growth, and modulating immune system by binding to endogenous zcytor18
                                                                                                 Cytokine receptor; Zcytori8; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; variant.
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/note- "wild-type Val 1s replaced with Ala"
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                                                                  Human cytokine receptor, Ecytor18 variant sequence.
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0; Mismatches
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N-PSDB; ABA95033, ABA95034.
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Cytokine receptor; Zoytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
                                                                    121 RIGHESOPELMAKFETDFEVKVVPFPSIKNESNYHPFFFRIRACDLILOPDNIACKPFWK 180
                                                                                                                                                ...61 TISQYACHDOVAVTILWSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPRQLNSSFR 120
                                          156 RIGHESOPELANKREIDYFVKVVPPPRINKESNYHPFFFRTRACDILLOPPRIACKPFWK (215
                                                                                                            181 PRINLAISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHBGPFRRKTCKQBQTTETTSCLLQ 240
                                                                                                                          RKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFL 360
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                                                                                                                                                                                                                                                                                                                            KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE
                                                                                                                                                                                                                                                                                                                                                                  Human cytokine receptor, Zcytor18 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07628 standard; Protein; 739.AA
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23-JUL-2001; 2001WO-US23253.
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The invention relates to an isolated cytokine receptor polypeptide designated. Exptor18. The Exptor18 polypeptides.can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell. Proliferation associated with psorlasis or tumour growth. The encoding nucleic acids are useful for providing Exptor18 in vivo by gene therapy, techniques: "Exptor18 injonucleotide. probes are useful for in vivo diagnosis, and the Exptor18 probes and primers can be used for in vivo diagnosis, and the Exptor18 probes and primers can be used to detect and localize Exptor18 gene: expression: in: titissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Exptor18 gene resides. The Exptor18 polyuncleotides can also be used in linkage-based testing of pulmonary: alveolar proteinosis, familial periodic fever and erythroleukemia; and erythroleukemia associated with holymorphisms of cytokine receptors. The present sequence represents a human Exytor18 splice variant.
                                                                                                      New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFK 120
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                                                                                                                                                                                                                                                                                   Claim 1; Page 102-106; 119pp; English.
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Best Local Similarity 98.1%
Matches 704; Conservative
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anti-ILI7rip antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human interleukin 17 (IL-17) receptor like protein described in the mathod of the invention.

738 AA;

Sequence

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anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
622 SQHGGLDQDGRARPALDGSAALQPILHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG 681.
                                                                                                                                             Interleukin.17; hIL-17 receptor like protein; immunomodulatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
             661 LSTDQTETSSLTESYSSSGLGEREPPALPSKLLSSGSCKADLGCRSYTDELHAVAPL 718
                            bone disease; vascular disorder; eye disorder; cancer; human
                                                                                                                       Suman Interleukin,17 (hIL-17) receptor like protein.
                                                                            AAU09904 standard; Protein; 738 AA.
                                                                                                              14-FEB-2002 (first entry)
                                              AAU09904;
                                                         RESULT 4
                                                                     AAD09904
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Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, 16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460. 15-MAR-2001; 2001WO-US08678 (AMGE-) AMGEN INC. WPI; 2001-611392/70. N-PSDB; AAS15346. WO200168859-A2. Homo saplens. 20-SEP-2001. Jing S;

useful for preventing, diagnosing diabetes, psoriasis and glaucoma

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These have Immunomodulatory, anti-infammatory, anti-diabetic, anti-infamilation of the immunosuppressive, hepatic, anabolic, anti-infamilation in the immunosuppressive, hepatic, anti-infamilation, dermatological, anti-infamilation, vascular, cytostatic, anti-infamilation, dermatological, or stepathic, vascular, cytostatic, anti-infamilation anti-infamilation in the interpretible or protein may be used to prevent and treat diseases associated with chotosin may be used to prevent and treat diseases associated with chotosin may be used to prevent and treat diseases associated with chotosin may be used to prevent and treat diseases associated with chotosin may be used to prevent and treat diseases associated with chotosin, infections (e.g. hepatitis and septicaemia), will dispertable in the fermination of the interpretible of constant and observed in the disperse and epilepsy), usefunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy), ung disorders (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. infermination meuropathy). The brast cancers, reproductive disorders (e.g. infermination neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify modulators of expression and activity. The sasays to identify modulators of expression and activity. The sasays to identify modulators of expression and activity. The 2; Page 152-154; 158pp; English. Claim

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182 RNINISQHGSDMQVSFDHAPHFGFRFFILHTKLKHEGPFRRKTCKQEQTTETTSCLLQN 241
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                                                                                                    62 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFKR 121
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                                                                                                                                                                  242 VSPGDIIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVWCR 301
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                            Gaps
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                                                                Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Interleukin 17 (hiL-17) receptor like protein substitution #3
                                                                                                                                                                                                                                                                                                                     DICGWRMKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT
                                                                                                                                                    122 TGMESQPFLMMKPETDTFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP
                                                                                                                                                                                                                                                                                                                                                      DPCGCEVALDLWEDPSLCREGOREWVIOKIHESQPIIVVCSKGMKIFVDKKNYKHKGGGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSTDELHAVAP 717
                            1; Indels 14;
 DB 22; Length 738;
Query Match 97.3%; Score 3725; Di
Best Local Similarity 97.8%; Pred. No. 0;
Matches 700; Conservative 1; Mismatches
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62 ISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 121

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The invention describes novel nucleic acids encoding interleutin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These contemporary anti-diabetic, anti-microbial, immunosuppressive, hepatic, anability, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anability, and extil-prakinsonian, anti-convulsant, anti-leakemic, anti-microbial, osteopathic, vascular, cytostatic, anti-leakemic, anti-microbial, osteopathic, vascular, cytostatic, anti-leakemic, anti-microbial, osteopathic, vascular, cytostatic, anti-leakemic, anti-microbial, and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat disease associated with claspropriate IL-17 receptor like polypeptide (ILI/TIP) expression. These include, for example immune discoders (e.g. inflammation, diabetes and transplant, rejection), infections (e.g. inflammation, diabetes and transplant, rejection), infections (e.g. inflammation, spincalarial, wight, discoders (e.g. acytic fibrosis, asthma and emphysema), skin disease (e.g. acytic fibrosis, asthma and emphysema), skin disease (e.g. stroke, and atherosclerosis and hypercalcaemia, welcome and breast cancer), reproductive discoders (e.g. infertinity and midgen in the productive discoders (e.g. infertinity and midgen in the productive therapy. The ILI/Tip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of smillar and activity. The antigens in the production of antibodies against the proteins and in assays to identify modulators of antibodies against the proteins and in assays to identify modulators of antibodies against the proteins and in antigens and antagonists may also be used as antigens in the production of antibodies against the proteins and in a surfactivity.
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Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 20.
                                anticonvulsanti anti-asthmatic; dermatological; renal; gateopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma
                                                                                                                                 hepatitis, anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disease; vascular disease; cancer; cye disorder; cancer; human; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- Ser, Thr, Ala, Cys
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28-NOV-2000, 2000US-0724460.
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-diabetic; immunosuppressive; anti-microbial; earti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostalic; anti-leukemnic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
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                                   122 TGMESQPFLNMRFETDYFVKVVPFPSIKNESNYHPFFFRTRACDILLQPDNLACKPFWKP
                                                             143 TGMESQPELNMKFETDYFVKVVPFPSIKNESNYBPFFFRTRACDLLLQPDNLACKPFWKP
                                                                                                                         (302 KKOOENIYSHLDEESSESSTYTAALPRERLRPRPKVPLCYSSKDGONHMIVVQCFAYFLQ
                                                                                                                                                                                                                                                                                                                                                                            482 NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHOFIDEEPDWFEK
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97.2%; Score 3721; DB 22; Length 738; 97.6%; Pred. No. 0; 1. Mismatches 2; Indels 14.

Best Local Similarity 97.6
Matches 699; Conservative

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Query Match

---GVGPASRNSGLYNITFKIDNCTTYLNPVGKHVIADAQNIT 82

2 DICCHEMIKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNIT 61

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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-i
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GSGRGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMD 481
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                                                                                                                                                         DFCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGR
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28-NOV-2000; 2000US-0724460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor. Ilke polypeptides useful as vaccines and in gene therapy. These have immunosuppressive, hepatic, anabolic, anotheratic, anti-alzehener's, renal, anti-parkinsonian, anti-convulant, anti-carbantic, dermatological, on the convulant, anti-convulant, and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding interleukin 17 recepter like polypeptides, secureful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psorjasis, and glaucoma.
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Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14;
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28-NOV-2000; 2000US-0724460.
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The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor. Itse polypeptides useful as vaccines and in gene therapy. These have immunosuppressive, ment-inflammatory, anti-dabetic anti-altelmer's, renal, anti-parkinsoilan, anti-incolan, anti-infertility and osteopithic, anti-incolar, anti-infertility and propting before and treat diseases associated with a population and before and proteins and before and proteins and before and anti-incolar, and anti-incolar, patients needing restorative therapy. The ILI/Trip may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ILI/Trip antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on thuman interleukin i? (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18. receptor like polypeptides, asthma, treating, e.g. leukemia, asthma, asthma, we have been asthma. Claim 18 : Page - : 158pp : English Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and diabetes, psoriasis and glaucomante (1) 表 1 元 二 元 元

Sequence 738 AA;

421 383. DFCGCEVALDLAEDFSLCREGORENVIORINESQFIIVVCSKGMKYFVDKKNYKHKGGGR 442 143 TGMESQPFLANKFETDTFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 202 182 RILINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQN 241 422 GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLAD 481 ISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR 121 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVALTVPLVVISAFATLFTVNCR 301 KKOQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361 83 2; Indels 14; Gaps DICGWRMKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPYGKHVIADAQNIT: 61 443 GSGKGELFLYAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLAD 362. DFCGCEVALDLMEDFSLCREGOREWVIOKIHESQFIIVVCSKGMKYFVDKKNYKHKGGGR 122 TGMESQPFLNMKFETDTFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP DB.22; Length 738; Best Local Similarity 97.0%; krec. nv. v. Matches 699; Conservative 1; Mismatches 97.1%; Score 3718; 97.6%; Pred. No. 0; Query Match 323 37 62 203 305 a . **g** ð 윱 셤 ö ä 셤 음 ó 유 · 8 å ö ò

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anti-dischemer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with

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Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma -

WPI; 2001-611392/70.

Jing S;

Claim 19; Page -; 158pp; English.

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anti-inflammatory; anti-diabetic; imminosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-astimatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachazia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                        11 FTR1 ELECTRICATION OF THE PROPERTY RESIDENCE AND THE PROPERTY RESIDENCE 
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                                                                                                                                                               563 QFVPPHPPPLRYREPVLEKFDSGLVLNDVACKPGPESDFCLKVEAPVLGATGPADSQHES
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482 NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFER
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28-NOV-2000; 2000US-0724460.
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inappropriate IL-17, receptor like polypeptide (IL17rlp) expression farese include, for example immune, disorders (e.g. inflammation, diabetes and transplant rejection); infections (e.g.; hepatitis and septicaemia). Use weight disorders (e.g. anorexia, cacheria and obesity), neuronal lung disorders (e.g. anorexia, cacheria and obesity), neuronal lung disorders (e.g. organication); infections, sating and openiasis, without sold sease (e.g. organication), without disorders (e.g., erzema.and.psoriasis, without dispercatements, vascular disorders (e.g., erzema.and.psoriasis, without disorders (e.g. infertility and miscariage); eye disorders (e.g. infertility and expected as and infertility in the infertion but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AM09904) 8888888888888888888888888888

Sequence, 738 AA;

122 TGMESOPPLANKFETDYFVKVVPPPSIKNESNYHPFFFRTRACDLLLOPDNIACKPFWKP 181 143 TGHESQPELNKREFIDEFVKVVPFPSIKNESKYHPFFRTRACDLLLQPDNLACKPFWKP 202 182 RNINISQHGSDMQVSFDHAPHNFGFRFFILHYKIKHEGPFKRKTCKQEOTIETTSCLLQN 241 242 VSPGDYIIELVDDTNTTRKVMEYALKPVHSPWAGPIRAVAITVPLVVISARATLETVMCR 301 GSGKGELFLVAVSAIAEKLRQAKQSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLAD 481. KKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361 362 DPCGCEVALDLWEDPSICREGOREWVIQKIHESQPIIVVCSKGMXYFVDKKNYKHKGGGR 421 62. ISQTACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGROCOQLILKDPRQLNSSFKR 121 NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNNHQFIDEEPDWFER 541 601 602 QHGGIDQDGEARPALDGSAALQPILHTVKAGSPSDMPRDSGIYDSSVPSSEISLPLMEGI 661 2 DICCWRMRAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLNPYGKHVIADAQNIT 61 Gaps 542 OFVPFHPPPLRYREPVLEKFDSGLÝLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES Query Match , 97.1%; Score 3718; DB 22; Length 738; Best Local Similarity 97.6%; Pred. No. 0; Matches 699; Conservative 2: 1. Mismatches 1.2; Indels 14; Ga Query Match Best Local Similarity 302 383 122 182 셤 8 셤 ð à 셤 ö à 8 용 ò 셤 ö 셤 ö 용 ð 셤 ö 셤 ò 셤

Interleukin 17; hill-17 receptor like protein; immunomodulatory; anti-falamatory; anti-falabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-laheincis; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; contrological; renal; osteopathic; vascular; contrological; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone; disease; vascular disorder; eye disorder; cancer; human; mutant; Buman Interleukin 17 (hIL-17) receptor like profein substitution #6. All the state of t Location/Qualifiers Misc-difference 515 AAU09956 standard; Protein; 738 AA. /label- Asp, Glu 16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460. 15-MAR-2001; 2001WO-US08678 14-FEB-2002 (first entry) Homo saplens. Synthetic. WO200168859-A2. 20-SEP-2001. AAU09956; nutein.

receptor like polypeptides, treating, e.g. leukemia, asthma, Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and diabetes; psoriasis and glaucoma WPI; 2001-611392/70.

(AMGE-) AMGEN INC.

Jing S;

Claim 23; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunoadulatory, anti-inflammatory, described in optibal activities. The In-inflammatory anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, anti-inflammatory, and propriate IL-IT receptor like polypeptide (IL)Tip) expression. These include, for example immune disorders (e.g. inflammation, disbetes and transplant rejection), infections (e.g. inflammation, disbetes and transplant rejection), infections (e.g. inflammation, disbetes and carried disorders (e.g. anorexia, cachexia and obesity), neuronal disorders (e.g. anorexia, asthma and emphysema), skin disease (e.g. eczema and psordasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. stroke and atherosclerosis, and hypercaloammatory), reproductive disorders (e.g. infertility and brancer), reproductive disorders (e.g. infertility and used as ্রউউর breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to defect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rip may also be used as

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662 STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSTIDELHAVAP 717

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antigens in the production of antibodies against the proteins and in sasays to identify modulators of expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity.
                                                       Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 23.
                                                                                                                                                                                                                                                       TGMESOPFLAMKFETDYFVKVVPFPSIKNESNYHPPFFRTRACDLLLOPDNLACKPFWKP 181
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                                                                                                                                        Query Match
Best Local Similarity 97.1%; Score 3718; DB 22; Length 738;
Best Local Similarity 97.6%; Pred No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps
                                                                                                                                                                                          NLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEK
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The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-infercibia,
containmondulatory, enti-inflammatory, anti-diabetic, anti-infercibia,
containmondulatory, enti-inflammatory, anti-diabetic, anti-infertility and
containmondulator, vascular, cytostatic, anti-interment, anti-infertility and
cophthalmological activities. The Li-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
cophthalmological activities. The Li-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
cinclude, for example immune discorders (e.g. inflammation, disbetes and
transplant rejection), infections (e.g. inflammation) discases (c.g. include, for example immune discorders (e.g. infections) disease, parkinson's disease and epilepsy),
displantion (e.g. cystic-fibrosis, asthma and emphysema), skin disease
(e.g. czema and psoriasis), kidney disease (e.g. glomerulonephritis),
bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
(e.g. stroke and arbanosierosis, andness (e.g. luckerility and
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
Drast cancer), reproductive dissorders (e.g. luckerility and
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
Commiscarriage, the presence of similar nucleic acids in samples and deentify
patients needing restorative therapy The III77tp may also be used as
antigens, in the production of antisodies against the proteins and in
antigens, in the production of antisodies against the proteins and in
antigens in the production of expression and activity. The
control of the control of the production of antisodies against the proteins are sequenced and artagonists may also be used to down regulate
Interleuxin 17, hir-if receptor like riotein; immunomodulatory; anti-inflammatory; anti-dispetic; immunomopuppessive; anti-uncrobial; hepatic; anabolic; anofectic; anti-alzhelmer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; optostatic; anti-latemamic; anti-infertility; ophthalmological; hepatitis; anorexis; cachexis; equipment dystunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
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Note: This sequence is not given in the specification but is based on thuman interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- Cys, Ser, Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for preventing, diagnosing
diabetes, psoriasis and glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2000; 2000US-189B16P.
28-NOV-2000; 2000US-0724460.
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Gaps

97.0%; Score 3714; DB 22; Length 738; 97.6%; Pred. No. 0; 1.1ve 1; Mismatches 2; Indels 14.

Best Local Similarity 97.6 Matches 699; Conservative

Human Interleukin 17 (hIL-17) receptor like protein substitution #5

(first entry)

14-FEB-2002 AAU09955;

AAU09955 standard; Protein; 738 AA

Similarity

738 AA;

Sequence Query Match

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DICGWRMKAAARPRI.CVANEGVGPASRNSGLINITFKIDNCTITLNPVGKHVIADAQNIT 61
                                     RNLNISQEGSDMQVSFDEAPENFGFRFFYLJHYKLKHEGPFKRKTCKQEQTTETTSCLLQN
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RESULT 11

AAU09957 standard; Protein; 738 AA.

AAU09957;

14-FEB-2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

anti-convulsant, anti-asthmatic; dermatological, renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; hépatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; muteln.

Homo saptens Synthetic Location/Qualifiers Misc-difference 602

/label- Cys, Ala,

WO200168859-A2

20-SEP-2001.

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15-MAR-2001; 2001WO-US08678.

6:MAR-2000; 2000US-189816P

28-NOV-2000, 2000US-0724460

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 24; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17

receptor like polypeptides useful as vaccines and in gene therapy. These
content of the work in the inflammatory anti-diabetic, anti-microbial,
immunosuppressive, hepatic, anabolic, anti-diabetic, anti-microbial,
anti-parkinsonlan, anti-formulaati, anti-asthmatic, dermatological,
contentation, vascular, cytostatic, anti-leukaemic, anti-inferility and
contemplation of the prevent anti-leukaemic, anti-inferility and
propriate IL-17 receptor like polypeptide (ILI/IL) expression. These
include, for example immune disorders (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. inflammation, diabetes
dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),
undight disorders (e.g. cystic fibrosis, asthma and obesity), neuronal
dysorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
(e.g. stroke and atheroscierosis, cancers (e.g. infertility and
bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders
(e.g. stroke and atheroscierosis, cancers (e.g. infertility and
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contents and an extensive t Note: This sequence is not given in the specification but is based on the human interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 24. anti-IL17rlp antibodies and antagonists may also be used to down regulate patients needing restorative therapy. The ILI7rip may also be used as amitges in the production of antibodies against the proteins and in assays to identify modulators of expression and activity rine. expression and activity.

738 AA; Sequence Score 3714; DB 22; Length 738; Pred. No. 0; 1; Mismatches 2; Indels 14; Gaps Query Match 97.0%; Best Local Similarity 97.6%; Matches 699; Conservative

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122 TGMESQPFLNMKFETDYFVKVVPPPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKP 181 ð

St 15/1

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"Tyrosine kinase phosphorylation site"

note- "N-myristoylation site" "N-myristoylation site" 'Glycosaminoglycan attachment site"

"N-myristoylation site"

"N-myristoylation site" "N-myristoylation site":

"N-myristoylation site"

"Tyrosine kinase phosphorylation site"

"Transmembrane domain" 1. 2.2.

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"N-myristoylation site"

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The sequence is PRO20026 which is the human interleukin 17 receptor, IL-17EH4, encoded by DNA 154095-2998. A composition containing ant/agonists to the PRO polypeptides or individual components are useful for treating a mammal with an 'immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropethy, systemic sclerosis, an idiopethic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic ansemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, contact dermatitis, an altergic disease e.g. food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Fig 18; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen J, Filvaroff E, Fong S,
Gurney AL, Li H, Hillan KJ,
Watanabe CK, Williams PM, Woo
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129..434
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N-PSDB; AAS09517.
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22-JUN-2000;
22-AUG-2000;
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18-FEB-2000;
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21-MAR-2000;
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                                                                                                  203 RNLNISQBGSDMQVSFDBAPHNFGFRFFYLHTKLKHBGPFKRKTCKQBQTTFTFSCLLQN 262
                                PORT AT VERGOTIELYDDINTERKYNHYALKPYHRADRAGPIRAVAITVPLVVISARATLFIVNCR 301
                                                            263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
                                                                                                                                                                                                                                               623 QRGGLDQDGEARRALDGSAALQPILHTVKAGSPSDNPRDSGIYDSSYPSSELSLPLMBGL 682
                                                                                                                                                                                                                               GSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFIØSCEGDVPGILDLSTKYRLAD 481
                                                                                                                                                                                                                                                                                          482 NLPQLCSHIHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLTVAICNMHQFIDEEPDWFEK 541
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phosphorylation site"
266.269
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147..150
/note= "Asn is N-glycosylated"
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19..24
/note= "N-myristoylation site"
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/note= "Asn is N-glycosylated"
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/note- *A
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Grimaldi CJ Vandlen RL;

J S, Goddard A, Godowski PJ, JJ, Tumas D, Van Lookeren M, Wood WI, Yansura DG;

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                    hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 polypeptide agonic, or antegonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.
                                                                                                                                                                                                                                                                                                                                               292
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                                                                                                                                                                                                  66 ACHDQVAVTILWSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPKQLNSSFRRTGME 125
                                                                                                                                                                                                                                          SOPPLANKEETDYFVKVVPPPSIKNESNYHPFFFRTRACDILLQPDNLACKPFWKPRALN 185
                                                                                                                                                                                                                                                                                                             ATLFTVMCRKKOGENIYSHLDEESSESSTYTAALPRERLRPRPRVFLCYSSKDGONHMNV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 GPADSQHESQHGGLDQDGEARPALDGSAALQPLIHTVKAGSPSDMPRDSGIYDSSVPSSE 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   653 LSLPLMEGLSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDEL 712
                                                                                                                                                                        7 RHKAAARPRICVÄNE-GVGPASRNSGIKNITFKYDNCTTYLNPVGKHVIADAQNITISQY
                                                                                                                                                                                                                                                                                                                                            ETTSCLLQNVSPGDY11ELVDDTNTTRKVMHYALKPVHSPWAGP1RAVA1TVPLVV1SAF
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                                                                                                      96.7%; Score 3703; DB 22; Length 728; 96.7%; Pred. No. 0; 14. 14. 14. 14. 2; Mismatches 8; Indels 14
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                                                                                                                            llarity 96.7%
Conservative
                                                                                                                       al Similarity
702; Conserv
                                                                                         Sequence 728 AA;
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The invention describes novel nucleic acids encoding interleukin (IL) 17

Treceptor like polypeptides useful as vaccines and in gene therapy. These
have immunoadulatory; anti-inflammatory, anti-diabetic, anti-alzheimer's, renal,
have immunoadulatory; anti-inflammatory, anti-diabetic, anti-alzheimer's, renal,
charlingsonlan, anti-convulsant, anti-asthmatic, dermatological,
anti-parkinsonlan, anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
proteins may be used to prevent and treat diseases associated with
proteins may be used to prevent and treat diseases associated with
control inappropriate IL-17 receptor like polypeptide (ILI/IL)p) expression. These
include, for example immune disorders (e.g. inflammation, diabetes and
cramsplant rejection), infections (e.g., hepatitis and septicacemia),
weight disorders (e.g. anticetions (e.g., hepatitis and septicacemia),
dysfunction (e.g. Alzheimer's disease, Parkinson's Titsease and epilepsy),
lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
(e.g. eczema and psoriasis), kidney disease (e.g. glomerutonephritis),
bone diseases (e.g. osteoporosis and hypercalcacemia), wasuular disorders
(e.g. stroke and atherosclerosis, cancers (e.g. infertility and
miscarriage), eye disorders (e.g. infertility and
and its complements may also used as diagnostic probes to detect and
cyclemia and the production of similar nucleic acids in samples and identify
patients needing restorative therapy. The III/TIP partipodies and antagonists may also be used as
antigens in the production of antibodies against the proteins and activity. The
contented in the production of similar misconsolope and activity m
                                   Interleukin 17; hIL-17.receptor: like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anti-orbital; anti-artimatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cochexia; neuronal dysfunction; lung disease; hepatitis; anorexia; cochexia; neuronal dysfunction; lung disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing; diagnosing and treating, e.g. leukaemia, asthma, diabetes, psoriasis and glaucoma
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interleukin 17 (hil-1) receptor-like protein version
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                                                                                                                                                                                                         disease; vascular disorder; eye disorder; cancer;
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 695; Conservative 1; Mismatches
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28-NOV-2000; 2000US-0724460.
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AAU10602 standard; Protein; 739 AA.

.14-FEB-2002 (first entry)

AAU10602;

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                                                                                                       81 ALGIEFLEGFRVILEELKSEGROCOOLILEDPROLNSSFRETGRESQPPLANGFETDYFV 140
                                                                                                                                           102 ALGIEFIKGERVILBELKSEGROCQOLILKOPRQLNSFRRTGWESQPFLNAKFETDYFV 161
                                                                                                                                                                                                                141 KVVPPPSIKNESNYHPFFFFTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHA 200
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gene therapy; protein therapy; lumunological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOHTROGSRRNIFRSKSGRSLYVAICHMHOFIDEEPDWFEKOFVPFHPPPLRYREPVLEK
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subunit (DCRS) polygeptides and the polynuclectides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label mannogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPRQLNSSFK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKKQOENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHANVVQCFAYFL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 ADTCSW-----XGVGPASRNSGLKNITFKXDNCTTYLNPVGRHVIADAQNI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ADTCGWRMKAAARPRICVANEGVGPASRNSGLYNITFKYDNCTTYLMPVGKHVIADAQNI 60
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to primate and rodent DNAX cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23; Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 25; 148pp; English.
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N-PSDB; AAS18134.
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ABB07630 standard; Protein; 739 AA.

ABB07630;

(first entry) 20-MAY-2002

Murine cytokine receptor, Zcytor18.

Cytokine receptor; Ecytori8; cell proliferation; antips pulmonary alveolar proteinosis; familial periodic fever erythroleukemia; chromosome 3pl4.3; gene therapy; mouse

W0200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001MO-US23253.

26-JUL-2000; 2000US-220747P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE,

Gao Z;

WPI; 2002-217048/27. N-PSDB; ABA95037, ABA95038.

to endogenous zcytor18 New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcyt

47.7

Claim 1; Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psorialsis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide, probes, are useful for in vivo disposis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The Zcytor18 polymorials in chromosome 3 in which periodic fever and erythroleukemia, and erythroleukemia, associated with pelymorphisms of cytokine receptors. The probes are polymorphisms of cytokine receptors. The probes is associated with mustic and erythroleukemia, associated with murine &cytor18 amino acid sequence

Sequence

1 ADTCGWRMKAAARPRICVANEGVGPASRNSGLYNITFRYDNCTTYLNP-VGKHVIADAQN 59 52; Indels 37; Mismatches Best Local Similarity Matches 611; Conservative

-GVGPASRNSGLHNITFRYDNCTTYLNPGGGKHAIADAQN 81

36 ADTCGWR

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83.8%; Score 3208; DB 23; Length 739; 84.6%; Pred. No. 1.3e-308; 739. AA; Query Match

CRKKQQENIYSHLDEESSESSTYTAALPRERLRPRVFLCYSSKDGQNHMNVVQCFAYF 359 LODFCGCEVALDLWEDFSLCREGGREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 419 GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVTFDFSCEGDVPGILDLSTKYRL 479 SRGEAGGEFFLVAVAAIAEKLRQAKQSSSAALRKFIAVYFDYSCEGDVPCSLDLSTKYKL 501 678 ITISQYACHDQVAVTILMSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSF 119 KPRNINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLL. 239 QNVSPGDYIIELVDDTNFTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVM 299 FERGEVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQ 598 929 LARGLSTDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDELHAVA 716 MONLPOLCSHLHSRDHGLOEP,-GOHTROGSRRNYFRSKSGRSLYVAICNMHQFLDEEPDW H--ESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP PL 718 9 20, 142 180 442 539 599 83 202 240 262 300 322 360 382 420 081 202 657 717 g á à 윰 셤 윱 ð 유 ō. ð Š a Š 셤 셤 ð ö 셤 ð ð

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw.model
Run on: May 19, 2003, 09:16:08 ; Search time 26,5067 Seconds (without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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275 GPIRAVAITVPLVVISARATLFTVMCRKRQQENIYSHLDEESSESSTYTAALPRERLRPR 334

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99.5	99.5	99	98.5	51	26.0	98.0	98 2.	.98	97.5	97.5	97 2.			'	cal protein		C; Accession: T42695	R;Bloecker, H.; Boecher, submitted to the Protein	A; Reference number:	Pře	type:	ss: 1-564 <a< td=""><td>mental sourc</td><td>LCB: DKFZp434N1928.1</td><td>. Match Local Similarity</td><td>563;</td><td></td><td> BPFFFRTRAC</td></a<>	mental sourc	LCB: DKFZp434N1928.1	. Match Local Similarity	563;		BPFFFRTRAC
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ubmitted to the EMBL Data Library, September 1999 Accession: T27282 Status: preliainary, translated from GB/EMBL/DDBJ	A, Accession: T30113 A, Status: preliminary: translated A, Molecule type: DNA A, Residues: 1-718 < CHIN A, Residues: 1-718 < CHIN A, Cross-references: EMRI: U3997: p
Molecule type: DNA Residues: 1-846 <mil> Cross-references: EMBL:AL110498; PIDN:CAB54470.1; CESP:Y64G10A.e. Cross-treferences: clone Y64G10A</mil>	C; Genetics: A; Gene: CESP: F56D1.2 A; Introns: 93/1; 121/2; 163/3; 459 C; Superfamily: Caenorhabditis eleg
Gene: CESP:V64G10A.e Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3 Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e	Query Match Best Local Similarity 20.6%; Matches 89; Conservative 68
Query Match 4.5%; Score 170.5; DB.2; Length 846; Best Local Similarity 21.4%; Pred. No. 4.1e-05; Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;	QY 280 VAITVPLVVISARATLFT
64 QTACHDOVAVTILMSPGALGIEFLKGFRVILBELKSBGROCOQLILKDFRQINSSFKRTG 123 - - - - - - - - - - - -	Qy 334 RPKVFLCYSKDGQNHMVVQCEA Db 414 FVKVMIVYAD-DNDLHTDCVKKLV
124 MESOPFLANKFETDTFVKVVPFPSIKNESNYHPFFFRTRACDLLLOPDNIAC-KPFWKPR 182 :::: : : : : :	QY 394 SQPIIVVCSKGHKYFVDKKNYKHK
183 NIMISQHGSDMQVSFDHAPHNEGFRFFILHTKLKHBGPFRRRTCRQBQTTFTTSCLLQNV 242 	QY 454 FIAVYEDISCEGDVPGILDLS
243 SPGDYIIELVDDINTTRKVKH-YALKPVHSPWAGPIRAVAITVPLVVISARATLFTVM 299 416	QY 511 NYFRSKSGRSLYVALCNHHQF :: :: Db 576 NVTQNISEAQIHEWNLCASRAMSR
300 CRKKQQENIXSHLDEESSESSTYTAALPRERLRPRYVFLCYSSKDGONHMNVVQCFAYF 359 	QY 562 DSGLVLMDVMCKPGPESDFCLKVE :
360 LODPCGCEVALDLWEDFSLCRECOREMVIOKIHESOFILIVYCSKGMKTFYDKRNYKHKGG 419 	Qy 622 LQPLLHTVKAGSPSDMPRDSGI DD 664 LQPHASHQNQPLILLPPEQCG-
420 GRGSGKGELFLVAVSAIAEKLRQAKQSSAALSKFIAVYFDYSCEGDVPGILDLSTKY-477 1 1 1 1 1 1 1 1 1 1	QY 680 GLGEERPPALPSK 692 Db 707 GEDPKTIVVK 716
478	RESULT 4 T09081
526 CNMHOFIDEEPDWFEK	telomere-associated recy-like hel. C;Species: Ustilago maydis (corn. C;bate: 11-Jun-1999 #sequence_rev C;Accession: T09081
555 EPVLEKF	R; Sanchez-Alonso, P.; Guzman, P. Genetics 148, 1043-1054, 1998 A; Title: Organization of chromosom

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A;Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 126.5; DB 2; Length 718;
Pred. No. 0.1;
58; Mismatches 165; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRP: 333
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                                      TEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAA 621
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egans.hypothetical protein.F56D1.2
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elegans cosmid F56DI.
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-	rans and	uji, E.; Hira	1 A	- Bacillus ha	submitted to the Protein A, Reference number: 21873 A.Accession. 717212	C; Accession: T17212 R; Poustka, A.; Klei	C; Date: 15-Oct-1999 #sequence				2 Db. 719	5 QY 508	5 0y 4 5 4	7 Db 613	407 407	Db 559 RCFWDSPFFIRSDGRQTASFALFDKLRREGGRNAIEVIDLSKTYRNRQVV	Qy 354	25 GO	8 8	Qy 235 TSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVVIS-AFA 6	. Db 472	OY 183 NINISOHG	aa.	QY 135 EIDYEVKVVPR-PSI	27. DD 37.2	OY 85 EFLAGERVILEBLASEGR	OY 26 ASRNSGIVITYFKINGTITINFVGRYTADADUTISOT ACHOUVANTIARSGALGI 1 1 1 1 1 1 1 1 1 1	Matcl	Query-Match (10) 752803.08; Soore 116.5; SPB 2; Flength Best Local Similarity 19.68; Pred No. 0.9;	A; Gene: BH1054	
A;Accession: F83781 A;Status: preliminary	Nucleic Acids Res. 28, 4317-4331, 2000 A/#141tel Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A/#6ference number: A83650, MUID:20512; PMID:11058132	C.Accession: F81781 R;Takani, B.:, Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Mucleic Acids Res. 28. 417-43312000	halodurans #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001	ter (ATP-binding protein) BH1054 [imported] -	RESOLT 5	Db 511 PPSE 514	Qy 689 IPSK 692	464	633	SGIGEREPPA	420 PGHHPQARGPGDOFHFTAPAQAGDPSTQGSRHPSMEGSSHPSMH	576 PESDPCIAVRANTICATOPADSOH RSOHGGI DONGER DDAINGS A TOUT BETWEEN	QY 516 KSGRSLYVALONMAQPIDEEDDWPEKQFYPFHPPPLRYREPYLEKFDSGLYLNDVMCKPG 575 The state of the second of the second sec	332 SQESGRAGEDGRPAESILLAGPQLDDRAP-ASGRASSAERGKVAPGADKEAMOLYRS	478	291 DWICGEGSPVIVATSA	DD 44/NILVECTSKELVARLAEMIGCAATSSESGSEADKAAIIQ 290	377 SLCREGOREWVIORIBESOFILVVCSKGMKTRVDKKNYKHKGGGRGS	DD 192 FISHNKITKPLIVRESTURSHICYSVRTAEHRMSGMTCTDAVRVVDECRARTDIW 246	OY 328 RERIRPREVELCXSKDGQHHANVYQCF-AYFLQDFCGCEVALDENEDF 376	132 YANRILLOOORLDRIVIDECHLILTARSYRRSHMOLAWHVRDVETGTWHLTARLPPIFEDA			III; CONSCEVALIVE 56; Mismatches 187; Indels 190; Gaps	3 1%; Score 117; DB 2; Length 757; 20.4%; Pred. No. 0.64; Live 56; Mismatches 187; Indels 190; Gans		And Angelia in the state of the	Residues: 1-75];	A; Status: preliminary, translated from GB/EMBL/DDBJ A; Wolecule type: DNA	Reference number: 4216557; WUID:98198830; PMID:9539423	

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DD 447 VPIVVPSQQAKPLRKORSAKET 468	RESULT 8 T04661 T04661 hypothetical protein F8D20.70 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 %sequence_revision 23-Apr-1999 %text_change 24-Nov-1999 C;Accession: T04661	R; Bevan, M.; Rose, M.; Hempel, S.; Entlan, K.D.; Jesse, T.; Heijnen, L.; Vos, submitted to the Protein Sequence Database, July 1998 A; Reference number: 2.15381 A; Accession: T04661 A; Molecule type: DNA.	AL031135 lltivar Columbia; BAC c 3/1; 274/3; 340/3; 373/	A; Note: F8D20.70 C; Superfamily: Arabidopsis thaliana hypothetical g Opery Match Opery Match Best Local Similarity 18:1%; Pred. No. 3; Best Local Similarity 18:1%; Pred. No. 3; Antches 154; Conservative 124; Mismatches	Qy 24 GPASRNSGLINITEKIDNCTTZLNPVGKHVIADAQNITISQYACHDQVA 72	QY 73 VIIMSPGALGIEFLKGFRVILEELKSBGRQCQQLILKDPKQLNSSFKRTGMESQP 128 :: :: :	OY 129 FLANKFETDYFEVKVVPPFSIKNESNHPFFFRTRACDLIAQPDNL, 173	OY 174 ACKPEWKPR-NIAISQHGSDMOVSEDHAPHNFGFRFFILETKL 215	QY 216 KHGDPEKRKTCKQEQTTETTSCLLQNVSPGDYILELVDD 254 :: : : : :	QY 255 TNTTRKVMHYALKPVHSPWAGBIRAVAITVPLVVISARATLFT 297	QY 298VMCRKRQDENIYSHLDERSESSTYTAALPRERLRPREVFLCYSSEDGO 347 : ::: : :	QY 348 NHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWV1QKIHESQFIIVVCS 402	QY 403KGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLR 441	QY 442 QAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNE 483	QY 484 PQLCSFLAGSDAGLQEPQQHTRQGSRRNTFRSKSGRSLTVAICNUAGPIDEEPD 537 1 1	
QY .486.LCSHLHSRDHGLQEPCQHTRQGSRRNYFRSKGRSLYVALCNMHOPIDEEPDWFEKQF 543 QY .486.LCSHLHSRDHGLQEPCQHTRQGSRRNYFRSKGRSLYVALCNMHOPIDEEPDWFEKQF 543 Db .163.AVSSGHYQCEKAADIAAGGTLTLRNDS9TSEAGRPSTHRFPLLPRRRG 210	OY 544 VPEH-PPPL		TRESULT 7 14.239 Vealcle transport protein - mouse	C.Species: Mus musculus (house mouse) C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 C.Accession: 149239 R.Tellam, J.T.; McIntosh, S.; James, D.E. J. Blol. Chem. 270, 5857-5863, 1995 J. J	A. Reference number: 149238; MUID:95197608; PMID:7890715 A. Accession: 149239 A. Fichus: preliminary; translated from GB/EMBL/DDBJ A. Molecule type: MRNA	A; Kesidues: 1.594 < KES> A; Cross-references: EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g642028 C; Genetics: A; Gene: munc-18c	Query Match 2.9%; Score 110; DB 2; Length 592; Best Local Similarity 18.5%; Pred. No. 1.6; Watches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;	QY 286 LVVISABATLETVMCHKKQQBNIYSHLDEESSESTYTAALPRERLAPRR 336 ::::	QY 337 VFLCYSSKDGQNHMNVVQCFAXFLQDFCGCE367 :	QY 368 -VALDLWEDFSLCREGOREMVIQKIHESOFILVVCSKGMKY 407	QY 408FVDKKNTKHKGGRGSGKGELFLVAVSAIAEKLROAKOSSSAALS 452 5	QY 453 KFIANYEDYSCEG-DVPGILDLSTKYRLADNLPQLCSHLH 491 :	QY 492 SRDHGLQEPGQHTRQGSRRNYFRSKSGRSLXVALCNMHQFIDEEPDWFEKQFVPFHPPPL 551	QY 552 RYREPULEKF	OY .586 AAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDWPRD-SGIY 644	

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Oy 431:VAVSAIAEKLEGARGSSSAALSKEIAVYEDYSCEGDVFGILDLSTKYR 478	Oy 564GLVLNDVMCKPGPESDFCLKVEAAVIGATGPADSÖGHESQHGGLDQDGEARPAL 616 Db 818 ASDVWSTGIVMWEVMS	protein kinase - mouse (fragment) (5) Species: Was musculus (house mouse) (5) Date: 03-Jul-1996 *Requence_revision 02-Jul-1996 *text_change 18-Jun-1999 (5) Accession: 149071 (5) Rivar, 3 C. 6. Conlon, F.L.; Robertson, E.J. (6) Mech. Dev. 48, 153-164, 1994 (7) A; Title: Identification of novel protein kinases expressed in the myocardium of the dage commer: 149071; MuID:95200798; PMID:7893599 (7) A; Accession: 149071 (7) A; Status: preliminary; translated from GB/EMBL/DDBJ (7) A; Residues: 1-938 < RES.	ff 18 Z; Length 938; 271; Indels 251; Gaps 42; -SRNSGLINITEKY 39 : : NSRTTSPAASICTCHNNFTRA 264	0. 0. 0. 0. 0. 0. 0. 0.
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217 HEGPERRYCKQBOTTETTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGP 1	OY 389 ORIHESOFI	Db 1137 DHLSQSKVAETELAKPLEDALLKYALGNHSADLDPGDFYPTEKSHPSEEVLSQPGDFS 1193 Qy 579 DFCLKVEAAVLGATGPADSQBSGGGLDQDGBARPALDG-SAALQPLLHTVK 630 Up 1194 EEAEDSQCCSLKLLGBEEGTEADSESNPEDGETQDDGVELPEAEGFSGSIVPRNLLESLT 1253 Qy 631 AG 632	4 HG 1 2 2 protei 11-Jan 110n: 1	J. Cell Biol. 142, 499-509, 1998 J. Cell Biol. 142, 499-509, 1998 J. Cell Biol. 142, 499-509, 1998 A.F. Cell Biol. 142, a novel zinc-finger CAG/Glutamine-repeat protein selectively locality. A.F. Cession: T42730 A.Scession: T42730 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-3942 ODIE> A.Cross-references: EMBL: 177034, NID: 93413809; PIDN: CAA76598.1; PID: 93413810 A.Experimental source: strain 129:SVJ	C; Genetica: 9F1 A; Map position: 9F1 A; Map position: 987 A; Map position: 987 A; Map position: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1 A; Note: bassoon C; Function: A; Description: may be involved in cytomatrix organization at the site of neurotransmi A; Description: conjouent of the presynaptic cytoskeleton C; Keywords: coiled coil; zinc finger	Ouery Match 2.84; Score 107.5; DB 2; Length 3942; Best Local Similarity 19.14; Pred. No. 41; Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11; Qy 481 DNLPQLCSHLHSPDGLQEPQGTRNGSRRNTFRERGRSLTYAICNHGFIDEE 535
OY 309 YSHLDERSSESTITAALPRENLEPREKVFLCYSSKDGQHHANVYQCFAYFLQDFC-GCE 367 DD 528	DD 600 VF.YALKTIKVGTTERQREDFISENSINGORDEPNIIRLEGUVTKSRVV 647 QY 479LADNILD-CCSHLERSDRGCQFT		PESTLT 11 T1360 protein homolog rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Accession: T13960 C;Accession: T13960 R;Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M. Submitted to the EMBi. Data Library, November 1998 A;Description: Dejetion in the beige gene of the beige rat due to recombination between A;Reference number: 217837	13960 iminary, translated from GB/EMBL/DDBJ iminary, ann 3788 cMOR> nces; EMBL:AB020019; NID:d1241953; PID:d1 source: strain DA; spleen	OMETY MATCH 2.84; SCORE 107.5; DB 2; Length 3788; Best Local Similarity 19.74; Pred: No. 39; Matches 142; Conservative 93; Mismatches 258; Indels 229; Gaps 38; QY 16 LCVANEGVGPASRNGLYNITERYDICTITINPYGRHYIADAQNITISGYA 66	DD 716 CNLIQAGNVIVQW

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A;Gene C;Key	A;Gene: dri C;Reywords: DNA binding; embryo		
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Result No.

	us-09-912-157-2_copy_36_753.rsp Page	OS MUS musculus (Mouse). CC Eukaryore; Metazos, Chor. OC Mammalia, Eutheria; Rode. OX NCBL_TaxID-10090; RN (1) RN SEQUENCE PROM N.A. RC TISSONE-Thymic 1 ymphoma; RX MEDLINE-96111968; PubMed	Caps' 34; RA Comeau M.R., Cohen J.I., Spriggs M.K.; Cohen J.I., Spriggs M.K.; RT Flerpestius Saimiri encodes a new cytokine, IL-17, which RT Flerpestius Saimiri encodes a new cytokine, IL-17, which RT Immunity 3:811-821(1955); RL Immunity 3:911-82(1955); RL Immunity 3:911-82(1955);	LRMLK 274 CC VISAF 292 DR :: VISAF 292 DR ILLVG 334 FT ILLVG 334 FT ILLVG 348 FT PT PDHL 390 FT LCSRG 404 FT LCSRG 404 FT CSRG 404 FT CSRG 404 FT CSRG 404 FT CSRG 406 FT CSRG 406 FT CSRG 407 FT CSRG	COLOR COLO	1 1 1 1 1 1 1 1 1 1
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-> VRFSELLMGGGRRLFHRSLLLRNSSLLSNALLPADT
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Best Local Similarity 20.1%; Pred. No. 0.008;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps
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SIGNAL
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EXTRACELLULAR (POTENTIAL):
EOTENTIAL.
CITOPLASNIC (POTENTIAL):
N.LINKED (GLCNAC...) (POTENTIAL).
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LFPLA -> SSPCL (IN REF. 2).
MISSING (IN REF. 2).
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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CDB87586FAAE49CC CRC64;
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Oncogene 19:2098-2109(2000).
Oncogene 19:2098-2109(2000).
Oncogene 19:2098-2109(2000).

ILINE. May play a role in controlling the growth and/or differenciation of hematopoletic cells.
OBGELLIATAR ACCATION: Type I membrane protein (1soform 1);
Secreted (1soform 2).

-I- ALTERNATIVE PRODUCTS: 2 1soforms; 1 (shown here) and 2; are produced by alternative splicing.

-I TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- MISCELLANDOUS: EVI27 is a common site of retroviral integration in BXH2 murine myeloid leukemias, localized near the ILI7BR gene. Proviral integrations result in increased expression of ILI7BR on
                                               NYFRSKSGRSLY --- VAICHMHQFIDEEPDWFEKQFVP-----FHPPPLRYREPVLEKF 561
                                                                                                                                                      562. DSGLVINDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAA 621
                                                                                                                                                                                                                                                                                                             622 LOPLIHIVKAGSPSDM--PRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSS 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09JFP3; 09JFP2;
15-5UN-2002 (Rel. 41, Created)
15-5UN-2002 (Rel. 41, Last sequence update)
15-5UN-2002 (Rel. 41, Last annotation update)
15-5UN-2002 (Rel. 41, Last annotation update)
16-5UN-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-2027323; PubMed-10815801; Jankins N.A., Copeland N.G., Inda E., Savyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shaughnessy J.D. Jr.; "Evi27 encodes a novel membrane protein with homology to the IL17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Alternative splicing.
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Sciurognathi; Muridae; Murinae; Mus
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalla, Eutherla, Rodentla,
NCBI_TaxID-10090;
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                                                                                                                                                                                                                                347, TICTETEFIQNECKSEVILEKWOKKKIARMGPVQWLATQKKAADKVVFILSNDVNSVCDG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 FIAVIFDYSCEGDVP---GILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRR 510
PRPKVFLCYSSKDGONHMN 351
                                                                                                                                                                            352 VVQCFAYFLQDFCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYPVDK 411
                                                                                                                                                                                                                                                                                                                                       412 KNYKHKGGGRGSGKGELFLVAVSAIAEKIRQAKQSSAALSKFIAVYFDYSCEGDVPGIL 471
                                                                                                                                                                                                                                                                                                                                                                                               280 VAITVPLVVISAFA-----TLFTVMCRKKOQENIYSHLDEESSESSTYTAALPRERLRP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 IAVVVLLILIIVLAVTGFGYVLWRDKVRSREVRNI--------ALTE 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 SQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSALAEKLRQAKQSSSAALSK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Last. sequence update)
01-FEB-1996 (Rel. 33, Last. amoutation update)
8TpOthetical, 81.6 kbs protein F5601.2 in chromosome II precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Mismatches 165; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. HYPOTHETICAL PROTEIN F56D1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
Chissoe S., Willson R.;
submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81622 MW; 42B9E056288417AA CRC64;
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WormPep; F56D1.2; CE01970.
Rypothetical protein; Transmembrane; Signal.
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Pred. No. 0.065;
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(Rel. 33, Last seq
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GNRTILIORDTIG -> TRENTEVTSGYPPAAKHQALKI SAPPLORPEDSYLLPPOPLASIZHDFYKLT (IN ISOFORN 2). 219		OY 286 LVVISAPATLET THE H H DD 34 INLIDERTIKLE
2.9%; Score 110.5; DB 1; Length 499; Similarity 24.1%; Pred.:No. 0.67; 0; Conservative 27; Mismatches 82; Indels 17; Gans 4;	<u> </u>	Oy 337 VFLCYSSKDGON 1: 1 Db 87 SVDCFLRDFGSN
CXSSKDGQHBMYVQCBAYELQDFCCCEVALDLAND 1	О П,	OY 368 -VALDIWEDFSI 11: 1 DD 147 VYTLDVPDAFYY
380 REGOREWICKIERSOFIIVVCSKGHKYFVDKKNYKHRGOGRGSGKGELFLVAVSALAEK 439 1372 ENGPVOHTAPOKOAADKVYFILESDYPTLCISACRARBGSARBUS-11FPIAPNIECSD 430	, ·	OY 408FVDKK DD 205 SKLAQLVEKKLE
440 LRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLADNLPQ 485		OY 453 KFIAVYFD 1::1 Db 253 TFQAMAYDLLP
-SSQTHLHRYLVVYLGGADLKGDYNALSVCPQ 462		OY 492 SRDHGLQEPGQE
COMMUNICACION		313
(Rel. 35,	- , н	Db 349 NIAEDCHREFKI
<pre>U.NOY-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3).</pre>		Oy 586 AAVIGATGPADS
Mus musculus (Mouse). Mustaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammala; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus. NCBL_raxID-10090;		645
SEQUENCE FROM N.A. MEDLINE-95197608; PubMed-7890715; Tellam J.T., McIntosh S., James D.E.; Molecular identification of two novel Munc-18 isoforms expressed in		RESULT 7 EPB3_HUMAN LID EPB3_HUMAN ST
J. Biol. Chem. 270:5857-5863(1995). [2] SEQUENCE FROM N.A.		
NETAIN-BALLYC; TISOB-BARDIN; MEDINE-96421662; PubMed-8824310; Gengyo-Ando K., Kitayama H., Mukaida M., Ikawa Y.; A murine neural-specific homolog corrects cholinergic defects in		DE Ephrin type-B rec DE kinase receptor E GN EPHB3 OR ETK2 OR OS Homo saplens (Hum
J. Neurosci. 16:6695-6702(1996)I-TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSEDI- SIMILARITY: BELONGS TO THE STXBP/UNC-18/SEC1 FAMILY.		
123		
use by program storiousactes institute. Institute at an or restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensealsh.ch.)		RA Strebhardt K., Ru RT "FCR medlated det RT 2.*;
EMBL; 030798; BAA19478.1; -:		C -1- FUNCTION: REC C EPHRIN-B1 AND C -1- CATALYTIC ACT
txbp3. 9; Seci- 1; 1.	·	tyrosine phos 2C -!- SUBCELLULAR I CC -!- TISSUE SPECIE CC -!- SIMILARITY: C
592 Aa; 67942 MW; 7874B71DE107871A CRC64;	_	C -1- SIMILARITY:

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22;
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                                                                                TVMCRKKQQ-----ENITSHLDEESSESSTYTAALPRERLRPRPK 336
                                                                                                                                                                                            HTROGSRRNIFRSKSGRSLIVAICNMHQFIDEEPDWFEKQFVPFHPPPL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...-DSGLVLADVMCKPGPESDFCLKVE 585
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                                                                                                                                                        NHEMNVYQCEATFLODFC----- 367
                                                                                                                                                                                                                                         SIC-----REGOREMVIQKIHESQFIIVVC----SKGMKY------ 407
                                                                                                                                                                                                                                                                         ...NIK--HKGGGRGSGRGELFLV----AVSAIAEKLRQAKQSSSAALS 452
                                                                                                                                                                                                                                                                                                                                                                                                                  -----YSCEG-DVPGIL----DLSTKYR-----LADNLPQLCSHLH 491
                                          Gaps
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EXERPOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO MD. -82.

CTIVITY: ATP + a protein tyrosine - ADP + protein companies.

CLOCATION: Type I membrane protein.

INCLITY: UBIGUITOUS.

CONTAINS 1 FAM DOMAIN.

CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                LISSCKMIDILEBGITVIENIKKNREPVROMKALFF-----ISPTER 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; PubMed-8397371;
Inch U., Wolf G., Luzius H., Grzeschik K.-H.,
Ruebsamen Waigmann H.;
etection of a new human receptor-tyrosine-kinase, HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 34, Created)
1. 34, Last sequence update)
1. 40, Last annotation update)
1. 40, Last annotation update)
1. 42, Last annotation update)
1. 48K-2)
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soa; Chordata; Craniata; Vertebrata; Euteleogtomi;
ria; Primates; Catarrhini; Bominidae; Bomo.
2.9%; Score 110; DB 1; Length 592;
lty 18.5%; Pred. No. 0.92;
servative 64; Mismatches 157; Indels 188;
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|PLRKDRSAEET 468
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SEQUENCE FROM N.A.
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between; the Swiss-Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                            entities requires a license agreement ((86e http://www.isb-sib.ch/announce)
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PHOSPHORYLATION (ADTO-) (BY SIMILARITY)
PHOSPHORYLATION (ADTO-)
(BY SIMILARITY)
PHOSPHORYLATION (ADTO-) (POTENTIAL).
PHOSPHORYLATION (ADTO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 122; Mismatches 301; Indels 250; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ADTCGWRMKAAARPRLC-----VANEGVGPA-----SRNSG-----LINITERY 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 DN-----CTTYLNPVGKHVIADAQNITISQYACHDQYAVTILMS-PGALGIEFLKGFRV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
ROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
ROSITE; PS50105; SAM_DOMAIN; 1::
ALBERTOR; PS50105; SAM_DOMAIN; 1::
ALBERTOR; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
GCOPLOR; Transmembrane; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109; 'DB 1; Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC. . .) (POT 57C82C397CC61103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDZ-BINDING MOTIF
                                                                                                                                                                                                                                                                                                  InterPro; IPR001090; Ephrin receptor.
InterPro; IPR001090; Ephrin receptor.
InterPro; IPR001961; FNLIII.
InterPro; IPR001962; FNLIII. repeat.
InterPro; IPR001660; SAM.
InterPro; IPR001665; SAM.
InterPro; IPR00145; "Kase_receptorV.
FAM.; PP000641; fn3; 2.
Pfam.; PP000641; fn3; 2.
Pfam.; PP00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119; TYPKC; 1.
00107; PROFEIN KINASE ATP; 1
150011; PROFEIN KINASE DOM; 1
100109; PROFEIN KINASE TER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      robom; PD000001; Euk_pkinase; 1.
robom; PD001495; Ephiln_receptor; 1.
                                                                                                                                                                                                                                                      110286 MW;
  * RECEPTOR SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%;
                                                                                                                                                                                                                               EMBL; X75208; CAA53021.1; -.
                                                                                                                                                                                                                                                                             HGNC: 3394; EPHB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00536; SAM; 1.
Pfam; PF01404; EPH_lbd; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 ' 4
998 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSITE: PS00109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSITE; PS00107
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199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eceptor; T:
IGNAL
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TRANSMEM
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ACT_SITE
MOD_RES
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431 VAVSAI----AEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLS---TKYR---- 478
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                                                                                                      208 FFYLHTKLKHEGPE-KRKTCKQEQTTETTSCLLQNVSP-GDYIIELVDDTNTTRKVMHYA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 QYSRPAEFETTSERGSGAQQLQEQLPLIVGSATAGLVFVVAVVAIAIVCLERQRH----- 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 LDEESSESSTTAALPRERLRPRPKVFLCTSSKDGQNHMNVVQCFAYFLQDFC-GCEVAL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | :: | | |: : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 DLWEDFSLCREGOREWVIOKIHESOPIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 GAGEFGEVCR-----GRIKQPGRREVF- 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521, LYV---AIC-----NMHQFIDEEPDWFEKQFVPFHPP-----PLRYREP----VLEKFDS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          764 ILVNSNLVCKVSDFGLSRFLEDDPS-----DPTYTSSLGGKIPIRWTAPEAIATRFTS 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 -----GLVLNDVMCKFGFESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 616
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----ROCOOLILKDPKOLNSSFKRTGMESOPFLAMKFETDYFVKVVPFPS 147
                                                                                                                                                                                                                                                                                                          148 -IKNESNYHPFFFRTRACDLLLOPDNLACKPFWKPRNLNISOHGSDMOVSFDHAPHNFGFR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LKPVH----SPWAGPIRAVAITVPLVVISAFATL-----FTVMCRKKQQENIYSH 311
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Busecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7227;
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PubMed-2554325; Streull M., Krueger N.X., Tsal A.Y.M., Salto H.; Afamily of receptor-linked protein tyrosine phosphatases in humans and Drosophila."; Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
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15-JUN-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphates posphatase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 TDQTETSSLTESYSSSGLGEEEPPALPSKLLSSGSCKADLGCRSTTDEL 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 PDITITITYGDMIN-MGRIK----ESFVSAGFASFDLVAQMIAEDL 965
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23;

Transport Control

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Iwal K., Minato N.;
"Human SPA-1 product selectively expressed in lymphoid tissues is a
"Human SPA-1 product selectively expressed in lymphoid tissues is a
specific Grease-activating protein for Rap1 and Rap2.";
J. Biol. Chem. 272:28081-28088(1997).
-1- FUNCTION: Gtpase activator for the nuclear ras-related regulatory
protein RAP-1A (KREV-1), converting it to the putatively inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 DHAPHNFGFRFFYL-----------------HYKLKHE--GPFKRKTC--- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 DVPKTPNGKVVSYLIHLLGNPMSTVDREMMGPKIRRIDEPHHKTLYESVSPNTNYTVTVS 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 -----KQEQTTETTSCLLQNVSPGDYIIELVDDFNTTRKVMHYALK---PVHSPWAGPIR 278
                                                                                                             Query Match 2.7%; Score 104; DB.1; Length 1462; Best Local Similarity 20.0%; Pred. No. 9.3; Matches 88; Conservative 53; Mismatches 136; Indels 164; Gaps Aatches 20 NEGVGPASR----NSGLYNITEKYD-----NCTYLNPVGKHVIADA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 -- SG-------FDKLKTAEDIFQONSRNLPYM--------PDKLKTATDYE-- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 -FRVRACSDLTK.---TCGP-WSENVWGTMDGVATRPINLSIQCHDNVTRGNSIAINW 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 ------CCIRLYLVRINNDNKELPDPEKLNIATYQEVHSDNVIRSSAITAEMIS 626
                                                                                                                                                                                                                                                                                   259 NDGNDPIQKFEITLQEAGFPIFTYHKDFINGSHTSTILDHFKPNTTYFLRIVGKNSIGNG 318
                                                                                                                                                                                                                                                                                                                                                                                                       319 OPTOYPOGITHEST -- DPIFIPKVETTGSTASTIFIGWNPPPPDLIDYIQYELIVSE - 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 KSECROCOQLILKDPRQLMSSFRRTGMESQPPLAMKFETDYFVKVVPPPSIKNESNYHPF 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 AITRHKKNGEPATGSCLMPVSTPDAIGRTMMSKVNLDSK---TVLKLYLPKISERNGPI- 578
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                                                                                                                                                                                                                                                                                                                                           Rubinfeld B., Munemiteu S., Clark R., Conroy L., Watt K., Croster W.J., McCormick F., Polakis P., Wolecular-cloning of a GTPase activating protein specific for the Krev-1 protein p2irel."; Cell 65:1033-1042(1991).
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Wai K., Minato N.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 755 755 % (POTENTIAL). (GLCNAC. . ) (POTENTIAL). 1462 AA; 167411 MW; %F8091D69E88230EB CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
Rapi GTPase activating protein 1 (Rapidab).
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MEDLINE-91256304; PubMed-1904317;
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P47736;
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                                                        tyrosine + phosphate.
- Succitudar Location Type I membrane protect.
- SIMILARITY: CONTAINS 2 IMMUNCHOBULIN-LIKE C2-TYPE DOMAINS:
- SIMILARITY: CONTAINS 2 FIRENOWCTIN TYPE III-LIKE DOMAINS:
- SIMILARITY: CONTAINS 2 PROFEIN-TROSINE PHOSPHATASE_DOMAINS:
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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FIBRONECTIN TYPE-III 2.
PROFEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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InterPro; IPR003600; Ig_like.
InterPro; IPR0000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00047; 19; 2. PF00102; Y_phosphatase; 2. 5; PR00700; PRTYPHPHTASE.
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PIR; B36182; B36182.
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613 RPALDGSAALQPLIATVRAGSPSDMPRDSGIYDSSVPSSELS		LESVSSSGTPHKRDSF1	694 LSSGSCKADLGC 7057 FF: 11.7	ENSULTA 10	BOUNDARY STANDARD; PRT; 859 AA. 012079: 013693: 013694:	15-TUL-1999*(Rel. 38, Created) 15-TUL-1999 (Rel. 38, Last: sequence update) 15-TUL-1999 (Rel. 38, Last: sequence update)	Active breakpoint cluster region-related protein. ARR.	Romo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nammalla; Eutheria; Erimates; Craniiii; Hominidae; Homo.	NCBI_TaxID=9606; [1]5	TISSUE-Hippocampus; MEDLINE-2406566f; PubMed-8262969; Tan RC. Ienior T., Manser B., Lim L.:	"The human active breakpoint cluster region-related gene encodes a brain protein with homology to guanine nucleotide exchange proteins	and GTPase-activating.proteins."; blol. Chem. 268:2729-27298(1993).	UENCE OF 39-859 FROM N.A. (LONG AND SHORT SUB-Fibroblast.	Heisterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J.; "Human ABR encodes a protein with GAPrac activity and homology to the	DEL nucleotide exchange factor domain."; J. Blol. Chem. 268:16903-16906(1993). [3]	SEQUENCE OF 436-597, FROM N.A. MEDLINE-20067847, Pubmed-2587217; Heisterkamp N., Morris C., Groffen J.;	"ABR, an active BCR-related gene."; Nucleic Acids Res. 17:8821-8831(1989).	-I- FUNCTION: GIPASE-ACTIVATING PROTEIN FOR MACHANIC CHOIS THE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, THEREBY ACTIVATING THEM.	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT-FORM; ARE PRODUCED BY TERNATIVE SPLICING. THOSE SHORT CONTRACTOR OF THE SPLICING.	-:- TISSEE SPECIFICATI; HIGHLY ENGINED IN INE BRAIN. NOON WEARDS:- EXPRESSION IN HEART! LONG:AND MOSCLE:- STWILMBETT: CONTAINS I DRI-HOMOLOGY (DB) DOMAIN.		-1- SIMILARITY: CONTAINS 1'RHO-GAP DOMAIN. -1- SIMILARITY: STRONG, TO HUMAN BCR.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS-Institute of Bioinformatics yand the EMBL outstation	-the European Bioinformatics Institute, There are no restrictions on its uses the indi-profit institutions as long as its content is in no way maddid and the statement to not removed "nears by and for commercial	entities requires a license agreement (see http://www.lab.slb.ch/announce/or send an enail to licensetlsb-slb.ch).	EMEL; U01147; AAC50063.1; EMEL; I19704; AAC37519.1; EMEL; II9704; AAC37519.1; AAC37519.1	EMBL) LISTOS; AMUSTOLOT; AUT_TAIT.
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	nral cortex and expressed of detected in the	-acetate (TPA) in	collaborat	are no restrictions on its its content is in no way sage by and for commercial	p://www.isb-sid.cn/announce/	-			A CRC64;	1; Length 663;	Indels 247; Ga	ACCOURTED COMMETTER STORY	FYLHYK	SLDTAIGHLVFSLKYD 119	ADDINITRKVMHYALKPVH 270 1	TSHLDRESSESTYTAALP 327	FVEFLE		KNYK	VPQDENTPFVPDMIASNFL 314	-KLRQAKQSSSAALSKFIA 456	AVFREPEELITELIN 371	GGLGEPGGHTRGGSRRNYR- 513	WFEKQFVPFHPPLR 552	KSPTRK	PADSQHESQHGGLXQDQEA 012 : P-DSGHVSQEPKSE 535	
-1. SUBCELLULAR LOCATION: Associated with Golgi membranes.	Kindney and panoreas. Abundant in the cerebral cortex and expand in the spinal cort. Not detected in the lymphoid tissues.	-1. INDOCTION: By 12-0-tetradecanoyiphorbol-13-acetate (TPA promyelocytic H1-60 cells -1. SIMILARIY: CONTAINS I RAFRAN-GAP DOMAIN.	his SWISS-PROT entry is copyright. It is prodetween, the Swiss Institute of Bioinformatics	the guropean Bloinformation institute, There are no restry use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and	ntities requires a license agreement (see nur r send an email to licenseelsb-sib.ch).	EMBL; M64788; AAA60252.1; Genew; ENC:9858; RAPIGAL	min, 0004. Interpro; IPR003109; GTPase_LGN. Interpro; IPR000331; Rap_GAP.	Pfam: PF02145; Rap_GAP; 1. Pfam; PF02188; GoLoco; 1. SMART; SM00390; GoLoco; 1.	GTFaae activation; Membrane. DOMAIN 210 397 RAP/RAN-GAP. SEQÜENCE 653 AB, 73391 NW, 3703B7CC603404DA CRC64;	2.78; 3/milarity 19.5%;	3; Conservative '80; Mismatches	132 MKFEIDYFVKVVPPPSIKNESNYHPFFFRTRACDLLLQPD	172NIACRPFWKPRILISQHGSDMQVSFDHAPHNFSFRE	71 PLOSPITKVKLECNPTARIYRKHFLGKEHFNYYSLDTALGHLV	215 LHEGPFKRKTCKOPOTTETTSCLLONYSPGDYIJELVDDTNTTRKVHHY 120 VIGDQEHLKLLARKKTYEDVIPISCLTEFNVVQAAKLVCEDVHVDR	271 SPWAGPIRAVAITVPLVVISARATLFTVMCRKKQOENITSHLDERSSESST 	174 YPKASRLIVTFDEHVISNNFRFGVIYQKLGQTSEEBLFSTNEESPA	328 RERLRPREVYELCYSKUGGNHANNVOCFAFFLQDFCGCEVALDLWEDF 1 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	301EGGREWVIQKIHESQFIIVVCSKGMKVFVDK	261 NKEIMFHVSTKLPYTEGDAQLQRKRHIGNDIVAVVPQDENTPFVPDM	416 HKLRGARGSGRGELFLVAVSAIAEKLRGARGSSSAA	315 HAYVVVQAEGGPDGPLYKVSYTARDDVPFFGPPLPDPAVFRGPEFQEFLLTKLIN	457 VYPOYSC-EGDVPOILDLSTRYRIANILPOILCSHHASRD-HGLQEPGOHTRQGSRRNYF- 1:1:1::1:1::1:1:1:1:1:1:1:1:1:1:1:1:1:	514RSKSGRSLYVAICHHGFIDEEPDWFEKQFYPF	429 ESFRRVIRSRSOSMDAMGLSNKKPNTVSTSHSGSFAPNNPDLAKAAGISLIVPP	553 IMEVLEKEDSGLYLNDVACKEGESDECLAVEARVLGATGEDSGHESQHGGLDQDOGA 1	
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                                                                                                                                                                                                                                                                                                     16-0cr-2001 (Rel. 40, Created)
16-0cr-2001 (Rel. 40,-Last, sequence update) ( 15-0cr-2002 (Rel. 41, Last, annotation update)
15-0un-2002 (Rel. 41, Last annotation update)
Guanine.nucleotide.releasing.protein (GNRP) (Ras-specific nucleotide
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Ammalia; Eutheria; Primates; Catarrhini; Rominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOUSTON TOWN TO THE EXCHANGE OF RAS-BOUND GDP BY GTP. SIMILARITY: CONTAINS 2 PH DOMAINS.
1. SIMILARITY: CONTAINS 1 DBL-BOOKOLOGY (DH) DOMAIN.
1. SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
1. SIMILARITY: CONTAINS 1 ROS-GEF DOMAIN.
1. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145381 MW; 86C6F54AA1E451F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1275 AA.
532 GYEVSKA------KTRVERDTAEPKWDEE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAS-GEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7 ... A. . .
                                                                                            デン が 八将品の様です。
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDS_CDC25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR001331; GDS_CDC24.
InterPro; IPR000048; IQ_region.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; \L26584; AAA58417.1; [-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RASGEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RasGEF;
                                                                                                                                                                                    GURP_HUMAN STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exchange factor CDC25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50096; IQ;
PROSITE; PS50003; PH_D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene. 151:279-284 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suanine-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterPro; IPR00189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID-9606;
                                                                                       PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fan;
fan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> MEESSEAIGLLDKVLEDEDVFLLEBCELGTPTSPGSGS
PFLVAVK (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEPLSHRGLPRLSWIDTLYSNFSYGTDEYDGEGNEEOKGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....IRAVAITVP-----LVVISAFAT-----LET--VMCRK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 YFVDKKNYKHKGGGRGSGKGELFLV********AVSAIAEKLRQAKQSSSAALSKFI 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALGIEFLEGFR----VILEELESEGROCOOL--ILEDPROLNSSFERTGMESOPFLNM-F 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 APGVEAGRGLEMRKLVLSGFLASEEIYINQLEALLLPMKPL----KATATTSQPVLTIQQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 FETDYFVKVVPFPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 IETIFY-----KIQDIYEIHKEFY------DALCPK------VQQW--DS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVTMGHLFQKLASQLGVYKAFVDNYKVALETAEKCSQSNNQFQKISEELKVKGP---KDS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 KQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGP----- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 KDSHTSVTMEALL-----YKPIDRVTRSTLVLHDLLK--HTPVDHPDYPLLQDALR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 ISONFLSSINEDIDPRRTAVTTPRGETROLVKDGFLVEVSESSRKLRHVFLFTDVLLCAK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 KOOENITSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 LKKTSAGKHQQYDCKWYIPLADLVFPSPEESEASPQVHPFPDHELEDMKMKISALKSEIQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 AVYPDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQH-----TRQGSRR 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VISNKDDDESPGLYGFLHVIVHSAKGFKQSANLICTLEVDSF 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 102; DB 1; Length 859; Best Local Similarity 20.5%; Pred. No. 6.4; Matches 117; Conservative 57; Mismatches 190; Indels 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor; Alternative splicing. DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R -> G (IN REF. 2).

RSKV -> VOGA (IN REF. 2).

L -> V (IN REF. 2).

9FD50CD54FA99483 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guanine-nucleotide releasing
DOMAIN 91 284
DOMAIN 301 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             859 AA;
                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      SMART,
                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
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SWISS-PROT entry is copyright; it is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AGLGQ------VLEFNYTAKLSLSPENVDDVLAVASFLQMQ-------DIVT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCKGELFLVAVSAIAEKLRQAKOSSS-----AALSKFIAVTFDYSCEGDVPGILDLST-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107. ACHTLKSLAEPSSTTGESADASAVEGGDKRAKDEKAATMLSRLGQARGSSSTGPGRELK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          523 VAICHWHOFIDEEPDWFEKOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCL 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476.KYRLMONLPQLCSHL-HSRDHGLQEPGQH-----TRQGSRRNYFRSKSGRSLY 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 EERGGQAESASSGAEQTEKADAPREPPP--------VELKPDPTSSMA- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 CGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSKGMK-YFVDKKNYKHKGGGRG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 CDCTFVVD-GVDF------KAHKA--VLAACSEYFKMLFVDQKDVVBLDISNA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                Wetal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 KVEAAVIGATGPADSQHESQHGGLDQDGEARPALDGSAALQPILLHTVKAGSPSDMPRDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches 146; Indels 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86664 MW; FFFB8E56EDEBF7ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   643 IYDSSVPSSELSLP---LAEGLSTDQTETSSLTESVSSSSGLGEE 684
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50097; BTB; 1.
PROSITE; PS50034; BTB; 1.
PROSITE; PS50034; BTC_INC_PINGER_C2H2_1; 13.
PROSITE; PS500157; ZINC_FINGER_C2H2_2; 13.
Iranscription regulation; DNA-binding; Einc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN REF. 2).
                                             CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6%; Score 99.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C2H2-TYPE
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ZINC FI
C2H2-TY
C2H2-TY
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                                                                                                                                                                                                                                                                                                                      ...cucum; PD000003; Enf_C2H2; 1...
SWART; SW00225; BTB; 1...
SWART; SW0nn=
                                                                                                                                                                                                                                             MGD; MGI:107410; :Zfp100.
InterPro; :IPR000210; BTB_POZ.
InterPro; :IPR000822; Znf_C2H2.
Pfam; PP00096; Zf-C2H2; 13.
Pfam; PP00651; BTB; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.6%;
                                                                                                                                                                                                  EMBL; U22396; AAA64848.1;
EMBL; U14556; AAA85493.1;
HSSP; P08046; 1A1H;
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                                PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muclear protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                           This
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                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last sequence update)
21nc finger protein 151 (Polyomavirus late initiator promoter binding protein (LP-1) (Zinc finger protein 131).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 311:219-224(1995).
-1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT REGULATES THE EXPRESSION OF SPECIFIC GENES.
                                                                                       91, RVILEELKSEGROCOOL-ILKD----PKOLNSSFRRTGME----SOPPLAMKFETDTFVK 141
                                                                                                           HTPHEHVERNSLDYA-----KSKLEELSR 421
                                                                                                                                                                                                                                                                                                                                                                                                                      | : | ::|::|
DISQIFVRQGSLIQVPMSEKGKITRGRLGSLEKEGERQCFLESKH-----LIICTRGS 506
                                                                                                                                                  142 VVPPPSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQ----HGSDMQVS-196
                                                                                                                                                                                 301. QIFYQGLKARISSWPTLVLADLLDILLP------MLAIYQEFYRNHQYSLQI- 346
                                                                                                                                                                                                               197 FDHAPHNEGFREFYLHYKLKHEGPFKRKTCKQEOTTETTSCLLQNVSPGDYIIELVD--- 253
                                                                                                                                                                                                                                   ---DINTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYS 310
                                                                                                                                                                                                                                                                                                                                         HIDEESSESTITAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCPAIFIQDFCGCEVAL 370
                                                                                                                                                                                                                                                                                                                                                                    IMHDEVSETENIRKNIAIERM -------GCEILL 451
                                                                                                                                                                                                                                                                                                                                                                                                  DLWEDF -----SLCREGOREWIOKIHESOFITWVCSKGM 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KYFVDKKNY------RGSGKGELFLVA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 GGKLHLTKNGVISLIDCTLLEEPESTEERKGSGODIDHLDFKIGVEPKDSPFTVILVA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 VSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLCSHLHS 492
51 - 524 - 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;
unusual arrangement of 13 zinc fingers in the vertebrate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rapp L., Carmichael G.G.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 RDHGLQEPGQHTRQGSRRNYFRSKSGRSLY 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CBA; TISSUE-Kidney;
MEDLINE-96003919; PubMed-7575457;
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ZNF151 OR ZFP100
Mus musculus (Mous
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15-JUL-1998 (Rel
15-JUL-1998 (Rel
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591 TESDTKEAQQHAVLHQESRTHQ------CS-------BCNHKSSNSSDLKRHIISV 633
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                                     . 96 ELKS----EGRÇCQQLILKDPKQLNSSFKRTGMESQP--FLNMKFETDTFVKVVPFPSIK 149
                                                                                                                                                 150 NESNYHPFFFRTRACDILILOPDNIACKPFWKFPRNINISORGSDWOVSFDHAPHNFGFRF 209
                                                                                                                                                                                                                                                                                 210 YLHYKLKHEGPPRKRICKQEQITETISCLLQNVSPGDXIIELVDDTNITRKVMHYALKPV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                   270 HSPWAGPIRAVAITVPLVVI---SAFATLFT----VMCRKRQQENIYSHLDEESSESSIY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 PSALKKHIRVHTGERPYECQTCEYKSADSSNLKTHIKSKHSKEIPLK----CDICL---L 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634 HTKAYPHKCDMCSKGFHRPSELKKHVATHKSKKMHQCRHCDFNSPDPFLLSHHILSAHTK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 YRLMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEP 536
                                                                                                     375 KSKKKKRPESKOYOSAIFVAPDGOT-----LRVYPCMFCGKKFKTKRFLK----RHIK 423
                                                                                                                                                                                                                                                                                                                                                                              449 - LHNHMESH----KLTIKTEKTTECDDC-RKNLSHA------GTLCTHKTMHTE---- 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 ------KGVNKTCKCKFCDYETAEQTLIAHHLLVVHRKK-----PPHICGECGKGFRH 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 TAALPRE-RLRPRPRVFLC----ISSKDGON---HMNVVQCFAFFLQDFCGCEVALDLWE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 DFSLCREGOREWVI---OKIHESOPIIVYCSKGMRYFVDKKNYKHKGGGRGSGKGELFLV 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       738 SGEKRHVISIHIKDYPHR-----GFRRPSE 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D., Pallavicini A., Lanfranchi G., Valle G.; "The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames."; Feast 13:261-266(1997).
                                                                                                                                                                                                                 Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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Bukaryote, Fungl, Ascomycota, Saccharomycotina, Saccharomycetales, Saccharomycetales, Saccharomycetaceae; Saccharomyces NCBL_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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DCP2 OR PSUI OR YNL118C OR N1917.
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MEDLINE-99438017; Pubmed-10508173;
Dunckley T., Parker R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97245296; PubMed-9090055;
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P53550;
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PROSITE; PSO1028; ZINC_FINGER_C2H2_2; 10.
Itanscription regulation; Activator; Zinc-finger; Metal-binding;
NNA-binding; Repeat; Nuclear protein.
OMAIN 372 382 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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Mammalla; Eutherla; Rodentia; Sciurognathi; Murlnae; Murlnae; Mus. N. NCBI Taxib-10090;
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19.2%; Pred. No. 9.5;
tive 74; Mismatches 207; Indels 210; Gaps
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                                                                       -i- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.
-i- SUBCELLAIAR LOCATION: NUCLEAT.
-i- STHILLARIT: BELONGS TO THE KRUEPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS. ZEX/ZEY SUBPAMILY.
                                                                                                                                                                                                                                                                             264 GTDS---GORLGMEGONLRSGTYGDRTESKAYGSIIHKCEDCGKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89168416; PubMed-2493989;
Mardon G., Page D.C.;
"The sac determining region of the mouse X chromosome encomposition with a highly acidic domain and 13 zinc fingers.";
Cell 56:765-770(1989)
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1722D1C23F019DF8 CRC64;
                                                                                                                                              783 AA.
                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 17. Last sequence update)
210-OCT-2001 (Rel. 40, Last annotation update)
210c finger T-chromosomal protein 2.
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C2H2-TYPE.
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                                                                                                                                                 STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86; Mismatches 182; Indels 218; Gaps 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 SLKIKSFAQLIKICPLVWRWDI--RVDEALQQFSKYKKSIPVRGAAIFNENLSKILLVQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 REWVIQKIHESQFIIVVCSKGMXYFVDKKNYKHKGGGRGSGKGELFLVA-VSAI----- 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 ------TIDDNQFI-------ERNIQGKNYK-------IFLISGVSEVFNFRPQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AEKLR--QAKQSSSAALSKFIAVYFDYS------CEGD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 VPGILDLSTKYRLMDNLPQLCSHLHSR------DHGLQEPGOHTR 505
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                    Cerevisiae and contains a functional; wutf motif: *
**AEGO. J. B15411-542(1999)
***AEGO. J. B15411-542(1999)
***AEGO. J. B15411-542(1999)
***AEGO. J. B15411-542(1999)
***AEGO. J. B2APING IS A THE MAJOR PATHARY OF HIGH DECAPING ENZYHE, BOUD DECAPING IS A THE MAJOR PATHARY OF HIGH DECAPATION IN TEAST. IT. CCCIRS. THENGUES DEADENTLATION, DECAPPING AND SUBSEQUENT IS STRONGLEDLITIC DECAY OF THE TRANSCRIPT BODY.
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**INITARITY: BELLONGS TO THE NUTH DEPLICATION OF THE TRANSCRIPT BODY.
**S. POMBE SPACI998.12.
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"The DCP2 protein is required for mRNA decapping in Saccharomyces. Cerevisiae and contains a functional; MutT motif.";
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        NUDIX BOX.

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        CONFLICT
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        SEQUENCE
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17.9%; Pred. No. 1
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PRINTS; PR00502; NUDIXFAMILY.
PROSITE; PS00893; NUDIX; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit thatitutions as long as its content is in no way modified and this statement, is not removed. 'Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20150255; PubMed-10684935; MEDLINE-20150255; PubMed-10684935; Mill S.R., Heldelberg J.F., Med T.D., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Heldman J., Khourl H., Craven B., Bowman C., Dodson R., Galtn M., Nelson W., DeBoy-R., Kolonay J., McClarty G., Salzberg S.L., Esten J., Fraser C.M., "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia.
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640 DSGIYDSSVPSSELSLPLMEGLSTDQ-----TETSSLTRSVSSSSGIGEEE
                                                                                                                                                                                                                                                                                         Chlamydla pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales: Chlamydiaceae: Chlamydophila.
NCBI_TaxID-83558;
                                                                                                                                               EXSE_CHLPN STANDARD; PRT; 1050 AA. 092/G7; 09381; 09K2F2; 30-MAY-2000 (Rel. 39, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
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EMBL; AE002164; AAE37903.1; ...
EMBL; AP002547; BAA98945.1; -.
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00580; UvrD-helicase; 1. e; Nuclease; Exonuclease; Endonuclease; Et; Complete proteome. 12	2.6%; Score 98.5; DB 1; Length 1050; Similarity 20.4%; Pred. No. 16; O; Conservative 85; Mismatches 201; Indels 181; Gaps	LEELKSEGROCOQLILKDPKQLNSSFKRTGMESQPPLNNKFETDYFVKVVP 144 :	FPSIKNESNYHPPFFFRTRACDLLLAPDNLACK	PENK-PRNIAISQHGSDMQVSFDHAPHNFGFRFFILHYKLKHGGFFKKTCKQ 228 	EQTTETTSCLLQNVSRGDIIELVDDINTTRKVMHYALKPV	GPIRAVAITVPLVVISAFATLFTVMCRKKQQBNIXSHLDEESSESSTYT 323 : :	AALPRERLRPRPRVFLCYSSKDGONHANVVQCFAYFLQDFCGCEVAL 370 :	DLWEDFSLCREGOREWVIGKIHESGFIIVVCSKGMKYFVDKRNYKHKGGGR- 421 :	GSGRGELFLVAVSAIAERLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDL 473	474 STKYRLMDNLPQLCSHLASRDAGLQEPGQHTRQGSRRNYFRSKSGRSLYVAI 525 	CNMHQFIDEEPDWFEKQFVPFHPPPLRYRE-PVLEKFDSGLVLNDVM 571
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Mammalla; Butheria; Primates; Catarrhini; Bominidge; Rongo....
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Bypothetical 63.1 kDa protein (Fragment).
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SEQUENCE FROM N.A.

FURTHAUGE M., Ind W., Ang S.L., Thisse B., Thisse C.;

Furthauge M., Lin W., Ang S.L., Thisse B., Thisse C.;

Sef is a feedback-induced antagonist of Ras/MAPR-mediated FGF agnalling...

Sagnalling...

Nat. Cell Biol. 4:170-174(2002).

EMBL; AF424804; AAL79530.1; -.
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Best Local Similarity 84,61
Matches 496; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       RPALDGSAALQPILHTVRAGSPSDNPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLT 672
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Buzchydanio rerio (Zebrafish) (Zebra danio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cyprinides;
Vyprinidae, Danio.
NCBL_TaxiD-7955;
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                                                                       IAEKLROAKOSSSAALSKRIAVIFOTSCEGOVPGILDLSTKYRLADNIAQLCSHIASRDH
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Tsang M., Friesel R., Kudoh T., Dawid I.;
"identification of Sef, a novel modulator of FGF signalling.";
Nat, Cell Hiol. 4:165-169(2002).
EMBL; ARJ64103; ARL/A6112.1; -
SEQUENCE: 745-AA; 83431 NW; 56FEIF089D98DDB4 CRC64;
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Last sequence update)
Last annotation update)
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Q80HJ9;
01-UUN-2002 (TEMBLFEL 21,
01-UUN-2002 (TEMBLFEL 21,
01-UUN-2002 (TEMBLFEL 21,
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544 VPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVL-----GATGPAD 596
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                                                                                                                                                                                   375 DFSLCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGGR-----GS 423
                                                                                                                                                                                                   395 HLEICKEGOMSWISRRIDEAHFIITVCSKGLKHFVERRHRGKATSKERNREPSASDSSS 454
                                                                                                                                                                                                                                              GRGELFLVAVSAIAEKLROAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKTRLADNL 483
                                                                                                                                                                                                                                                               POLCSHLHSRDHGLQEPGGHTROGSRRNTFRSKSGRSLYVAICNWHQFIDEEPDWFEKQF 543
                                                                                                                                                                                                                                                                                                                           SQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLP 656
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                                                                             275 SINTERGEOTHYSQVESPWACPIRMAITYPLVIMSAFATLFTVACRKRODENITSHLDE
      195 VSFDHAPHNFGFRFFILHYKLKHEGPFKRKTCKQEQTTETTSCLLQNVSPGDTITELVDD
                                  215:VVFDHAPSTFGFSIYYLYKLRQEGPFRLKRCKPEQNGPKTTCVLQDVTPGTXAIELRDD
                                                               TNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDE
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MEDLINE-99069613; PubMed-9851916;
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Science 282:2012-2018(1998).
EMBL; AL110498; CAB54470.1;
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                                                           375 DESICREGOREMYIQKIHESOFIIVVCSKGMKYEVDKKNYKHKGGGR------GS 423
                                                                                  2.395 HIRICKEGOMSWILSRRIDEAHFIITVCSKGIKHFVERRHRKGKATSKEKNREPSASDSSS 454
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OY ... 315 ESSESTITAALPERFERENT SKYFLCTSSKOGONHAWWOCFAYFLODFCGCEWALDIAME 374
                          335 ESSESSSQTTALSADRPRPRIFICESRDGAKHLAVIQSFAFFLQDFCGCEVSLDLWE 394
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                       424 GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNL
                                                                                                                                              PQLCSHLHSRDHGLQEPGQHTRQGSRRNTFRSKSGRSLYVAICNNHQFIDEEPDWFERQF
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MEDLINE-21824237; PubMed-11802165;
Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
"Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
                                                                                                                                                                                                                                                                                                                                                                    LAEGLSTDOTETSSLTESVSSSSGLGEREPPALPSKLLSSGS-CKADL 703
                                                                                                                                                                                                                                                                                                                                                                                      Fuerthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBLs, AF40132; AAL78817.1; - EMBLS, AF40132; AAL78817.1; - 3EQUENCE 745 AA; 83437 MW; 75BB9EDCC08A4652 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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64 QYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGROCOOLILKDPRQLNSSFKRTG 123
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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11.4%; Pred. No. 2e-06;
ve 82; Mismatches 225; Indels 211;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                           339 ...-NFIDIELDIDLIPSVIPIESAHD....--GRC-LCVIENGCSCLADWKPV 382
                                                         183. NINISQHGSDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTETTSCLLQNV 242
                                                                                        243 SPGDYIIELVDDINTTRKVMB-YALKPVHSPWAGPIRAVAITVPLVVISAFAIL--FTVM 299
                                                                                                                                                  416 ------WHIYA------ITGGAIIAILENCAGLKCYKKE. 445
                                                                                                                                                                                  300 CRKKOGENIISHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHANVVQCFAYF 359
                                                                                                                                                                                                     360 LQDPCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 419
                                                                                                                                                                                                                                                             420 GRGSGKGELFLVAVSAIAEKLROAKOSSSAALSKFIAVYFDYSCEGDV--PGILDLSTKY 477
                                                                                                                                                                                                                                                                                                                                                                                       592 THRKYVEPPINKLLQYSIP----NSLMTMTTALFEQPARPEQLAGENQVFAR----LQAAI 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRKLNYIESDPOWFENTHHRVATRRVSELEAHNIVPL-PPSLEVRVEDEDAFGOMETLPI 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPVLEKR------DSGLVLNDVMCKPGPESDFCLKVEAAVEGATGPADSQHES 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 DELKEKFAAKROLEVEVILDSEDVKILEDVRCAPGP----IHVEPTEPEVLEPAEEPMEE 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 QRGGLDQDGEARPALDGSAA----LQPLL-HTVKAGSPSDNPRDSGIYDSS-VPSSELS 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            759 AEED-EEDEDDVDSVEGQTARIEELQRLIVH-----KDMANDSGNLDSAXVSGSDFS 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 VANEGVGPASRNSGLYNITFKIDNCTT----TLNPVGKHVIADAQNITISQYACHDQV 71
                                                                                                                                                                                                                                                                                                                              526 CNMHOFIDEEPDWFEK-------OFVPFHPPPLRYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loljens J.C., Anderson R.A.,
"Type I phosphatidylinositol-4-phosphate 5-kinases are distinct
nembers of this novel lipid kinase family.";
D. Biol. Chem. 271:32937-33943(1996).
EMBL: U78576; AAC50911.1;
Interpro: IPP002499; PIPSK.
EMBL: PR01504; PIPSK.
SWART; SM00330; PIPKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.1%; Score 117.5; DB 4;; Length 562;
Best Local Similarity 18.1%; Pred. No. 0.083;
Matches 133; Conservative 105; Mismatches 239; Indels 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 AA; 62633 MW; ABE7988EB73506A0 CRC64;
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MEDLINE-97115834; PubMed-8955136;
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.7.1.68).
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                                                                                         -----PYASGMPIRKIGHRSVDSSGETTYKKTTSSALKGAIQLGTHTVGSLSTKPER 106
                                                                                                                                                                   131.NMKFETDYFVKVVPFPS----IKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRILNI 186
                                                                                                                                                                                                                           143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 RTLLPRFYGLYCVQAGGKNIRIVVMNNLLPRSVKMHIKYDLKGSTYKRRASQKEREKPLP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 KVFLCYSSKDGQNHANVVQCFAYFLQDF-CGCEVALDLWEDFSLCREGQREWVIQ--+KI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 HESQFIIVV-----CSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLR 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 RGGTMETDDHMGGIPARNSKGERLLLYI------GIIDILQSYRFVKKLEHSW 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 KALVHDGDTVSVHRPGFTAERFOR------FMCN-----TVFKK--IP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 FHPPPLRYREPVLEKFDSGLVLNDVMCKFGFESDFCLKVEAAVLGATGPADSQHESQHGG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 LKPSPSK------KFRSG---SSFSRRAGSSGNSCITYQPSVSG-----EHKAQ--- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYD----SSVPSSELSLPLMEGL 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....VTTKAEVEPGVH---LGRPDVLPQTPPLEEISEGSPIPDPSFS-PLV-GE 539
                                                                                                                                                                                               SQHGSDMQVSFDHAPHNFGFR---FFY-------LHYKLKHEGPFKRKT
                                                                                                                                                                                                                                                                                                                 196:VQHKEAB-----PLQKLLPGYYM------NLNQN------P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHI.-HSRDH-GLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVP
1 MASASSGPSS-SVGFSSFDPAVPSCTLSSAASGIKRPMASEVLEARQDSYISLV----
                                                                                                                                                                                                                                                                                                                                                                                     CKOEQTTETTSCLLQNVSPGDY11ELVDDTNTTRKVMBYALKPVHSPWAGPIRAVAITVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q-------AKQSSSAALSKPIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanchez-Alonso P., Guzman P.;
Organization of chromosome ends in Ustilago maydis: reco-like helicase motifs at telomeric regions.";
Genetics 0:0-0(1998).
EMBL; AF030885; AAB95264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_raxID-5270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 AA
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01-JAN-1998 (TrEMBLrel. 05, Last seqt
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 TLOMLTISTILEKL 553
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85 EFLKGFRVILEELKSEGR------QCQQL--ILKDPKQLNSSFKRTGMESQPFLNMKF 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 ARDFRVYECESCEGCPFRPECTRARGNRQVHYNPVY------EELKAKQHQKLK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCF---AFFLODECGCEVALDLWEDFSLCREGOREWY----IQKIHESQFILVVCSKGNK 406
                                                                                                                                                                                                                                                                                                                             Query Match 3.0%; Score 116.5; DB 16; Length 901; Best Local Similarity 19.6%; Pred. No. 0.21; Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TSCLLQNVSPGDYIIELVDDTNTTRKVMHTALKPVHSPWAGPIRAVAITVPLVVIS-AFA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 KRATVDRRSKEPKNTNQHKNREN----------------------SIKRF-----SIKRF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 TFVDRKNYRHKGGGRGSGKGELFLVAVSAI-----AEKLRQAKQSSSAALSK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 MFIERGEMVGLLGPNGAGRSTTISMISSLIQPTSGDVLIRGGSIHKOSKAIRSILGVVPQ 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ESVHIELGLVALAHNLR 524
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                                                                                                                                                                                                                                                                                                                                                                                                            26 ASRNSGLYNITERYDNCTTYLNPVGKHVIADAQNITISQY-ACHDQVAVTILWSPGALGI 84
genome sequence of the alkaliphilic bacterium Bacillus and genomic sequence comparison with Bacillus subtilis.";
                                            NUCLEIC ACIDS Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 NINISQHG-----SDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 ----SEEGRILYQKRKTDVESVFGHVKQNLGFRRLHLRGK-----SEEGRILYQKRKTDVESVFGHVKQNLGFRRLHLRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 TLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRRVFLCYSSKDGQNHMNVV
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01-DEC-2001 (TrEMBirel. 19, Last amnotation update)
68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68).
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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                        ATP-binding; Transport; Complete proteome.
SEQUENCE 901 Aa; 104585 MW; E519406E650B2CBB CRC64;
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                       halodurans and genomic sequence compa
Nucleic Acids Res. 28:4317-4331(2000)
                                                                                                                                                                                                                                                     PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                        ERBL; APO01510; BAB04773:1;
InterPro; IPR003593; RAA_ATPase.
InterPro; IPR001439; ABC_transportr.
InterPro; IPR002559; Transposase_11.
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01-MAY-1997 (TrEMBLrel. 03, Last seq
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Pfam; PF01609; Transposase_11; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 ------GSSHPSSHGSSHPSIHGSSHPSIHGSS-HPSIHGSGOHGGORRKQOPD 510
                                                                                                                                                                                                                                    233 ETTSCLLONVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAV----AITVPL-- 286
                                                                                                                                                                                                                                                            287 ------VYISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALP-----327
                                                                                                                                                                                                                                                                                                                                                                                         --RERLRPRPRVF-----LCYSSKDGQNHMNVVQCF-AYFLQDFCGCEVALDLWEDF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SICREGOREWVIOKIHESOFIIVVCSKGMKYFVDK-----KNYKHKGGGRGS------423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGIL--DLSTKY 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 SQESGRAGRDGMPAESILLAGPQLDDRAP-ASGRASSAERGRVAPG---ADKEAMQLYRS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 KSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVLEKFDSGLYLNDVMCKPG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 PESDFCLKVEAAVLGATGPADSQH---ESQHGGLDQDGEARPALDGSAALQPLLHTVKAG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            633 SPSDMPRDSGIYDSSVPSSE-LSLPLMEGLSTDQTETSSLTESVSSS---SGLGEEEPPA 688
                                                                                                                                                    ttch, 3.1%; Score 117; DB 3; Length 757; 2al Similarity 20.4%; Pred. No. 0.15; 111; Conservative 56; Mismatches 187; Indels 190; Gaps
                                                                                                                                                                                                                                                                                                                                                   132 YANRILOOORLDRIVIDECHITLTARSYRRSMMOLAWHVRDVETOTVWIJATLPPIFEDA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FRON N.A.
SEQUENCE-125 / JCM 9153;
MEDLINE-2012582; Pubhed-11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales,
Bacillaceae, Bacillus.
NCBL_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNI-2002 (TrEMBLrel. 21, Last annotation update)
Transposase (08)/ABC transporter (ATP-binding protein).
BH1054.
                                                                                                                  757 AA; 84382 MW; 1AE1E414435382A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 AA.
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    IPR001650; Helicase_C.
                                        ; helicase_C; 1.
                                                         SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                            ATP-binding; Helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         689 LPSK 692 ·
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Horikoshi K.;
    InterPro;
                                                                                                                    SEQUENCE
                                                                                                                                                          Query Match
                                                                                                   NON_TER
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A ELBERGER J., Soehl G., Willecke K.;

A ELBERGER J., Soehl G., Willecke K.;

The structural and functional diversity of connexin genes in the mouse grand human geneme.;

The structural and functional diversity of connexin genes in the mouse stand human geneme.;

The structural and functional diversity of connexin grand human geneme.;

EMBL: AJ414564; CAC93846.1;

DR FROSTEP: PRO0029; CONNEXING.1;

DR PROSTEE; PSO0407; CONNEXING.1;

DR PROSTEE; PSO0409; CONNEXING.2; UNKNOWN.1.

SQ SEQUENCE 370 AA: 40140 AW; CD49F31743AFFC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 DGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVP---SSELSLPIMEGLSTDQTETSSLTE 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 PGARA-----GGEGAGSPRRTSRVSG--ETKIPDEDESEVISSASEKIGR-QPRGRPHRE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%; Score 111.5; DB 4; Length 370; Best Local Similarity 28.9%; Pred. No. 0.16;44
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565 LVINDVMC-----KPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 616
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery: Match 28.9%; Score 111.5; DB 4; Length 348; Best Local Similarity 28.9%; Pred. No. 0.14; Matches 43; Conservative 25; Mismatches 56; Indels 25;
                                                                                                                                                                                                                                                                                                              Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121749; CAC10186.1; -
Interpro; INDOS00; Connexin.
PRAM; PR00029; CONNEXIN.
PRAM; PR00206; CONNEXIN.
SAMAT; SM00037; CAN. I.
PROSITE; PS00407; CANNEXINS.1; 1.
PROSITE; PS00408; CONNEXINS.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1.348 AA; 37805 MW; 07EB6478067F8995 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     096KN9;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                        01-MAR-2001 (TrEMBLYel: 16, Last sequence update) 01-JUN-2002 (TrEMBLYel: 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA
                                                                                                                    3A425A6.2 (Similar to connexin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 SVSSSSGLG-EEEPPALPSKLLSSGSCKA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 AAGDPRGSGSEEOPSAAPSRLAAPPSCSS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                   NCBI_TaxID-9606;
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096KN9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 PYASGMPIKKIGHRSVDSSGETTYKKTTSSALKGAIQLGITHTVGSLSTKPERDVLMQDF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 YFVKVVPFPS----IKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101, YWESIFFPSEGSNLTPAHHYNDFRFKTYA------130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 QVSFDHAPHNFGFR---FFY-------LHYKLKHEGPFKRKTCKQEQTT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 -----AKQSSSAALSKFIAVTFDYSCEGDVPGILDLSTKYRLMONLPQLCSHL-HSR-493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367. DDHNGGIPARNSKGERLILIYI------GIIDILQSYRFVKKLEHSWKALVHDG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 DIVSVHRPGFTAERFOR------FMCN------TVFKK--IPLKPSPSK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 YREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEA 612:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 ------EHKAG----SSPSRRAGSSGNSCITYQPSVSG-----EHKAQ-------481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 RPALDGSAALQPLLHTVKAGSPSDMPRDSGIYD----SSVPSSELSLPLMEGLSTDQTET 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79. PGALGIEFLK-GFRVILEELKSEGROCOQLILKDPKQLNSSFKRTGMESOPFLANKFETD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 PVAFRIFRELEGIRPDDYLISLCSEPLIELCSSGASGSLFT-VSSDDEFIIKTVQHKEAE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293. ATLPTVMCRKKO------OENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYS. 34.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 YGLYCVQAGGKNIRIVVNNNLLPRSVKMHIKYDLKGSTYKRRASQKEREKPLP----T 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343. SKDGQNHMNVVQCFAYFLQDF-CGCEVALDLWEDFSLCREGQREWVIQ---KIHESQFII 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 VV-------CSKGMKYFVDKKNYKHKGGRGSGKGELFLVAVSAIAEKLRQ-----442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 SIHNIDHAQREPLSSETQYSVDTR----RPAPQKALYSTAMESIQGEARRGGTMET 366
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.9%; Score 112.5; DB 4; Length 549;
Best Local Similarity 18.1%; Pred. NO. 0.23;
Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 DH-GLOEPGOHTROGSRRNYFRSKSGRSLYVAICNMHOFIDEEPDWFEKOFVPFHPPPLR
                                                                                                               MEDITIVE-97115834; PubMed-8955136;
MEDITIVE-97115834; PubMed-8955136;
LOIJens J.C., Anderson N.N.;
Type T. phosphatelylinositol-4-phosphate 5-kinases are distinct members of this novel lipid kinase family.";
                                      Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                348 AA.
                                                                                                                                                                                                                              Chem. 271:32937-32943(1996):
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J. Biol. Chem. 271;32937-329
EMBL, U78575; Asc50910.1; -.
Interpro: IPR002498; PIP5K.
Pfam., PP01504; PIP5K.
SMART; SM00330; PIPKc; 1.
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Q9H460
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	SO.	Arabidopsis
SSELSLPLMEGL	8888	Eukaryota, Vi Spermatophyta eurosids II;
SYSSSOLG-EEEPPALDSKILLSSOSCKA 701 I 1 Hit Hall the stall to a second stall the stall to the second stall the stall to the second stall the stall the second st	8 8 8 8 8	[1] SEQUENCE FROM KOEtter P., 1
	# # E	Submitted (J
6. PRELIMINARY, C. S. PRT 1283 428	8 8 a	
01-CCT-2000 (TrEMBLrel. 15, Created) 1.28	2 % %	
01-DEC.2001.(TERMELTAL. 19, Last annotation update)	2 2 3	EU Arabidops Submitted (M
UNEXESSAKALL. Rumo sapiens (Human). Enterrorts : Motascas (Mordata: Cramista: Vortobrata: Dutalacetomic.	888	
Mammaila: Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	តីត ត	
N.A.	S S	
-	,	Query: Match
Well B., Wellenfeuther K., Gassenhuber W., Boecher M., Bloecker H., Bauersachs S.		Matches . 154;
Lauder V., Udesternoett A., Beyer A., Acenter A., Strack N., Machine B.W., Ottenweelder B., Obermaier B., Tampe J., Heubner D.,	δ.	24 GPASR
Manuotic K., Aoid B., Aleid M., Pouetka A.; Tywards a Catalog of Human Genes; and Proteins: Sequencing and	<u>,</u> 8	148 GKASRVY
Analysis of July Movel Complete Fronein Coaing Human cunas.; Genome Res, 11:1242-435(2001).	ΦŽ	73 VTILWSP
Embly ALLIANT (MD30304.2) EMPOCHEICAL PROCESS. ENGREENE ADD AN. AEAA MW. BASEBANIADERS ORGE.	<u>a</u>	208 LFVLGKS
12 5 4 5 4 5 4 5 4 5 4 5 5 5 5 5 5 5 5 5	ď	129 FLIMKFE
Pred. No. 0.27;	đ	268 LLNLSDE
KLRQAKQSS-SAALSKFIAVYFDISCEGDVPGILDLSTKYRLADNLPQ 485	VO.	174 ACK
: :: PRGPASSHCQLTLSSSKTVSEDRPQ	a	
486 LCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDREPDWFEKQF 543	&∵ €	216 KH
163 AVSSGHTQCERAADIAPGQTLTLRNDSSTSEASRPSTHKFPLLPRRRG 210	3 . 8	25.5
544 VPPH-PPPLRTREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAA 587	2 6	. 446
	δo.	298
- SGKKBRP	셤	
641 SG-IYDSSVPSSELSLPLARGLSTDQTETSSLTESVSSSGLGEREPPALPSKLLSSG 697	0	
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	δ i	6 03
KESULT 13 ID 1091789 PRELIMINARY: PRF: 917 AA	8 8	5/4 ITSLAHV
; -1998 (TrEMBLrel, 08, Created)	: A	631
01-NOV-1998 (TEMBLrel. 08, Last sequence update) 01-UN-2002 (TEMBLrel. 21, Last annotation update)	δ ·	484 PQLCSHI
orocein.	8	
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37;
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databases.
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Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
ta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae;
Brassicales; Brassicaeae; Arabidopsis;
3702; Marsicaeae; Arabidopsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KGMKTEVDKKNTKHKG-----GGRGSGKGELFLVAVSAIAE----KLR 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SSAALSKFIAVYFDYSCEGD------VPGILDLSTKYRLMDNL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHSRDHGLQEPGQHTRQGSRR----NYFRSKSGRSLYVAICNMHQFIDEEPD 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGALGI -- EFLKGFRVILEELKSEGROCOQLILKDPKQLNSSFKRTGMESQP-- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PEWKPR-NLNISQHG-----SDMQVSFDHAPHNFGFRFFYLHYKL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
                                                                                                                                       Bevan M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NSGLYNITFKYDNCTTYLNPVGKHV---IADAQNI--TISQYACHDQVA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHHYALKPUHSPWAGPIRAVAITVPLVVISAFATLFT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETDY -----FVKVVPFPSIKNESN---YHPFF-----FRTRACDLLLQPDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BGPFKR-----KTCKQBQTTETTSCLLQNVSP-TT--TGBYITELVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 110; DB 10; Length 917;
larity 18.1%; Pred. No. 0.87;
Conservative 124; Mismatches 281; Indels 292;
                                                                                                       J., Jesse T.,
Schueller C., B
                                                                                                                                                                                                                                                      OM N.A.

1818 sequencing project;

MAR.2000 to the EMBL/GenBank/DDBJ databases.

1135: CAA20026.1;

135: CAA20026.1;

187: CABBORATO.1;

180: WD40; 2.
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10; WD40; ....
1 protein; Repeat; WD repeat.
317 Aa; 101552 MW; 1809BDC42302C820 CRC64;
                                                                                                   DM N.A. S., Entlan K.-D., Hohelsel Fempel S., Entlan K.-D., Hohelsel Vos P., Mewes H.W., Mayer K.F.X., UL-1998) to the EMBL/GenBank/DDBJ
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Buman; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; PRO20026; DRA 154095-2998; systemic lupus erythematosus; rhemmatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease; degreestins demyelinating disease; degenerative cartilaginous disorder; transplantation associated disease. 19.~24 /note- "N-myristoylation site" 38.41 /note- 'Asn is N-glycosylated' 56.59 /note- 'Asn is N-glycosylated' "Asn is N-glycosylated" 147..150 /note= "Asn is N-glycosylated" 182..185 /note= "Asn is N-glycosylated" "Asn is N-glycosylated" Human Interleukin 17 receptor, IL-17R84 Location/Qualiflers AAU04958 standard; Protein; 728 AA CARGOLLESSEN, (first entry) 113 .116 /note- *A Modified site Modified-site Modified-site Homo sapiens. **Kodified-site** Modified-site Modified-site Region

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idiopathic inflammatory myopathy; Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease; a demyelinating disease, an autoimmune or immune-mediated skin disease; contact dermatitis, an alteriot disease e.g. food thypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polymeuropathy. Treating a degenerative cartilaginous disorder comprises administering a prolist prolypeptide agoing; or antegonist to the mammal. Numerous examples of the diseases and disorder care given in the specification.
                                                                                                                                                                                                                                                                                                                                                                             311 RKKQQENIYSHLDESSESSSTYTAALPRERLRPRPRVFLCTSSKDGQHEMNVVQCFAFFL 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 LSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSTTDELHAVAPL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2210; DB 22; Length 728; 100.0%; Pred: No: 1.7e-210; Indels 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M; Vandlen RL;
Watanabe CK, Williams PM, Wood WI, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes -
                                   Title . . Cal
 S CAMP/GMP:dependent protein kinase 389
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N-PSDB; AAS09517.
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10-NOV-2000;
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18-FEB-2000;
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Interleukin 17; hill-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-afronial; hepatit; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; anti-asthmatic; dermatological; renal; osteopathic; hepatitis; anorexia; cachexia; auti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular diseace; eye disorder; cancer; human.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S;

15-MAR-2001; 2001WO-US08678;

Homo sapiens. W0200168859-A2 20-SEP-2001;

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The invention relates to primate and rodent What cytokine receptor submuit (DCRS) polypeptides and the polyuncleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The submuits may also be functional immunogens to elicit recognising antibodies, or antigens capable of shidning antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisers or antibodies apable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogencial receptor. This sequence represents the human DCRSS
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                                                                                                                                                                                               Claim 1; Page 25; 148pp; English.
(SCHE), SCHERING CORP.
                                                                                                       WPI;;;2002-106198/14.
N-PSDB; AAS18134.
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322 RKKQQENIYSHLDEESSESSTTTAALPRERLRPRPRVFLCTSSKDGQNHANVVQCFAFFL 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10602 standard; Protein; 739 AA.
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(strange 2002) (first entry)

电视器器器器器

AAU10602;

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor-like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammartory, anti-diabetic, anti-antener's, renal, anti-parkinsonian, anti-inflammartory, anti-diabetic, anti-infertility and optically anti-covulaint, anti-eachmart, dermatological, costeopathic, vascular; cytostatic, anti-leukaemic, anti-infertility and proteins may be used to prevent and treat diseases associated with proteins may be used to prevent and treat diseases associated with a proteins may be used to prevent and treat diseases associated with a proteins may be used to prevent and treat diseases associated with a proteins any be used to prevent and treat diseases associated with the proteins (e.g. inflammation, diabetes and transplant rejection), infections (e.g. inflammation, diabetes and transplant rejection), infections (e.g. inflammation, diabetes and cransplant rejection), infections (e.g. harkinson's disease and epilepsy), but disorders (e.g. alrohen and obesity), neuronal dystuction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), but disorders (e.g. cystic fibrosis, asthma and emphysems, asthma and emphysems, asthma and emphysems, and disorders (e.g. growed disorders (e.g. glomerillity and theoremsis), kidey disease (e.g. glomerillity and theoremsis), kidey disease (e.g. glomerillity and theoremsis (e.g. infertility and theoremsis (e.g. infertility and theoremsis may also used as disquostic probes to detect and catagonists may also be used as antigens in the production of antibodies adainst the proteins and interneurs of expression and activity may also be used to down regulate antigened and activity may also be used as antigens in the production of antibodies adainst the proteins and activity may also be used to down regulate antigened and activity and antagonists may also be used to down regulate correllation. ö Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukaemia, asthma, the invention. 9 - 228.

Note: Residues 1-288 of this sequence correspond to residues 8-296 of sequence shown in AAU10601 which is incomplete in the specification. 1 RKKOOENIYSHLDEESSESTYTAALPRERLRPRPRVFLCYSSKDGONEMNVVQCPAYFL 60 Query Match 100.0%; Score 2210; DB 22; Length 739; Best Local Similarity 100.0%; Pred. No. 1.8e-210; Matchés 418; Conservative 0; Mismatches 0; Indels 0; useful for preventing, diagnosing diabetes, psoriasis and glaucoma Claim 2; Fig 1; 158pp; English. मार्थस्य भवतः । WPI; 2001-611392/70. N-PSDB; AAS16201 Sequence

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121 RGSGRGELFLVAVSAIAEKLRQARQSSSAALSRFIAVYFDYSCEGDVPGILDLSTRYRLM 180
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RESULT

ABB07628 standard; Protein; 739 AA.

ABB07628;

zerski zouz (first entry)

Cytokine receptor; Zcytori8; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; splice variant. Ruman cytokine receptor, Zcytor18 splice variant.

Homo sapiens.

WO200208259-A2

31-JAN-2002.

23-JUL-2001; 2001WO-US23253.

26-JUL-2000; 2000US-220747P.

(ZIMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE,

WPI; 2002-217048/27; N-PSDB; ABA95035, ABA95036.

New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 Claim 1; Page 102-106; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated Scytoria. The Scytoria polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic soids are useful for providing Scytoria in vivo by gene therapy techniques. Ecytoria oligomucleictide probes are useful for in vivo diagnosis, and the Scytoria probes and primers can be used to detect and localize Ecytoria gene expression in tissue asmiples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Scytoria gene resides. The Scytoria polypurcleotides can also be used in

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linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytori8 splice variant.
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RESULT

ABB07626 standard; Protein; 753:AA.

ABB07626;

XX 2003 Of Glass 20 3 (first entry)

Human cytokine receptor, Zcytor18 amino acid sequence.

Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy.

#0200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US23253

26-JUL-2000; 2000US-220747P.

(ZYMO) ZYMOGENETICS INC.

S S Presnell SR, Kuestner RE,

WPI; 2002-217048/27. N-PSDB; ABA95031, ABA95032.

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor

: A (3):

/label- V750A //octe- "wild-type Val is replaced with Ala"

TELEFANISOOD STATE

WO200208259-A2.

26-JUL-2000; 2000US-220747P. 23,JUL-2001; 2001WO-US23253.

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The invention relates to an isolated cytokine receptor polypeptide...

Casignated Ecytoris The Ecytoris polypeptides can be expressed by the standard recembinant methodology. The polypeptides can be used to inhibit coil proliferation associated with postiasis or tumour.growth. The groot cell proliferation associated with postiasis or tumour.growth. The groot cell proliferation associated with postiasis or tumour.growth. The groot cell proliferation associated with providing Ecytoris in vivo by gene therapy techniques. Ecytoris oligonolectide probes are used to detect and localize Ecytoris probes and primers can be used to detect and localize Ecytoris probes and primers can be used to detect and localize Ecytoris gross aberrations. The probes are also useful for detecting gross aberrations. The horizonesome is in which, and localize fewer and ecytoris polymoriol@tides can also be used in linkage; based testing of pulmonary alveolar proteinosis, familial and polymorphisms of cytokine receptors. The present sequence represents a human Ecytoris and organized with
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modulating immune system by binding to endogenous zcytor18
                                                  336 RKKQOENIYSHLDESSSSSSTTAALPRERLEPREKTVFLCTSSKDGONHWAVVQCFAYFL 395
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Matches 418; Conservative 0; Mismatches 0; Indels 0;
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                                                                                    Claim 1; Page 2; 119pp; English.
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designated & Cytor18. The zeytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit estandard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psorlasis or tumour growth. The encoding nucleic acids are useful for providing Ecytor18 in vivo by gene therapy techniques. Ecytor18 oilgonucleotide probes are useful for in vivo diagnosis, and the "zcytor18 probes and primars can be used to detect and localize Ecytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which

New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytor18

Presnell SR, Kuestner RE, Gao S; (ZYMO) ZYMOGENETICS INC.

7. · · · ·

N-PSDB; ABA95033, ABA95034.

2002-217048/27.

Disclosure; Page 94-98; 119pp; English.

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Ecytoris gene resides. The Ecytoris polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Ecytoris variant amino acid sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180
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Human cytokine receptor, Zcytor18 variant sequence.

(first entry)

20-MAY-2002

ABB07627;

ABB07627 standard; Protein; 753

Location/Qualifiers Misc-difference 269

Homo saplens

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361 LSTDQTETSSLTESVSSSSGLGEEEPPALPSKILSSGSCKADLGCRSYTDELHAVAPL 418 ö 셤

RESULT

AAU09904 standard; Protein; 738 AA

AAU09904;

14-FEB-2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein.

Interleukin 17; hIL-17 receptor like protein; fimunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbia; hepatic; anabolic; anorectic; anti-alrheimer's; anti-parkinsonian; anti-convulsant; anti-sathmatic; dermatological; renal; osteopathic; avascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human.

Homo sapiens.

W0200168859-N2. THE RESERVE 15-MAR-2001; 2001WO-US08678

16-MAR-2000; 2000US-189816P 28-NOV-2000; 2000US-0724460

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70. N-PSDB; AAS15346.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 2; Page 152-154; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, costeopathic, vascular, cytostatic, anti-straming anti-infertility and optibal mological activities The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with circulde, for example immune disorders (e.g. inflammation, diabetes, and transplant rejection), infections (e.g. hepatitis and septicaemia), we wight disorders (e.g. antimared), and obesity), neuronal cyfunction (e.g. Alzheimer's disease, parkinson's disease and emphysema), extendidanders (e.g. cystic fibrosis, asthma and camphysema), extin disease (e.g. eczema and psoriatis), kidney disease (e.g. glomerulonephritis), condiseases (e.g. serioders (e.g. eczema and psoriatis), kidney disease (e.g. glomerulonephritis), condiseases (e.g. serioders), reproductive disorders (e.g. effective), missioners, condiseases (e.g. disease), and hypercalcaemia), vascular disorders (e.g. stroke and atheroscierosis, cancers (e.g. infermia, myeloma and characters), resproductive disorders (e.g. infermia, myeloma and construction. anti-III]7rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI/IIp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The

ö receptor like protein described in the method of Gaps. 382-ODFCGCEVALDLWEDFSLCREGOREWYLOKTHESOFILVVCSKGMKYFVDKKNYKHKGGG 441 121 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180 DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE 240 502 DNIPQLCSHLHSKDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVALCHMHQFIDEEPDMFE 561 241 - KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300 SQHGGIDQDGEARPAIDGSAALQPILHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG 360 61. ODFCGCEVALDIMEDFSLCREGOREMVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGG 120 622 SORGGLODGEARPALDGSAALQPLLHTWYRAGSPSDWPRDSGIYDSSVPSSELSLPLAGG-681 1 RKKOGENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFFL 60 LSTDQTETSSLTESVSSSGLGEBEPPALPSKLLSSGSCKADLGCRSTTDELHAVAP 417 682 LSTDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGSCRADLGCRSYTDELHAVAP 738 Oquery Natch Park The Title 99,64,74 Score 2201,58 DB:22;74 Length 738; Best Local Similarity 199,84; Pred: No. 1.46-209;14 Charles 416;27 Conservative 120; 2415 matches 5117 /Indels: 0; Security of the second Sequence 0.738.AA; Nov. 104.800 the invention: . I'V Interleukin 17 181 301 361 á ୍ଷ୍ଟିଷ୍ଟ ଓଡ଼ à ā ò 셤 ö 8 à 용 à 셤 Š 음 à . 음

AAU09951 standard; Protein; 738 AA.

AAU09951;

4 TO THE STATE OF THE COLLY)

Human, Interleukin 17 (hiL-17), receptor like protein-substitution #1

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anti-parkins anti-alrahmer's; anti-parkinsonian; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; disease; neuronal dysfunction; lung bone disease; vascular disorder; eye disorder; cancer; cachexia; anorex1a; repatitis; nutein.

Romo sapiens. Synthetic.

/label- Gly, Pro or Ala Location/Qualiflers Misc-difference

WO200168859-A2

20-SEP-2001.

15-MAR-2001; 2001WO-US08678.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

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Itng S;

(AMGE-) AMGEN INC

WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 18; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleutin (IL) 17 ceceptor like polypeptides useful as vaccines and in gene therapy. These have immunomedulatory, anti-inflammatory, and inflammatory, and inflammatory, and inflammatory, and include, for example immune disorders (e.g., harbatharia and septicaemia), include, for example immune disorders (e.g., napratory), and appropriate Ti-inflammatory, and inflammatory, and and disorders (e.g., ancreais, asthma and obesity), neuronal or weight disorders (e.g., ancreais, asthma and obesity), neuronal or equilibrial and phypercal campais, and phypercal campais, and appropriates (e.g., ancreais, and hypercal campais, and appropriates (e.g., ancreais, cancers (e.g., glaucoma and policibrial), kidney disease (e.g., glaucoma and appropriate disorders (e.g., qlaucoma and retinal neuropathy). The observation expension of anti-inflammatory and infarility and edect and quantitate the presence of similar uncleic acids in samples and indentify andilators of expression and activity. The anti-orders and antaponiates may also be used as anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory. The complements of expression and activity and anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory. The anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory. The anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory. The anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory and anti-inflammatory. the Note: This sequence is not given in the specification but is based on thuman interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18.

Sequence 738 AA;

0; Gaps 99.6%; Score 2201; DB 22; Length 738; 99.8%; Pred. No. 1.4e-209; 1.4e-0; Mismatches 1; Indels 0; Query Match 99.6 Best Local Similarity 99.8 Matches 416; Conservative

- 1 RKKOGENIYSHIDEESSESSTYTAALPRERLRPRPRVFLCYSSKDGONHMAVVQCFAYFL 60 ö
- ODFCGCEVALDLWEDFSLCREGGREWVIOKIHESOFIIVVCSKGMKTFVDKKNYKHKGGG 120 გ ö
 - 121 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180 382

용 ä 윱

- 442
- ð 셤
- 241 KQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300 562. RQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCRPGPESDFCLKVFAPVLGAFGPADSQHE 621 à 셤
- 301 SQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDNPRDSGIYDSSVPSSELSLPLAMEG 360 ð
- 361 LSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP 417

682

The state of the s

RESULT 9

The Control of the Co 952 AAU09952 standard; Protein; 738 AA.

AAU09952;

14-FEB 2002 (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #2.

Interleukin 17; hit-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-inframmatory; hepatic; anti-organical; anti-asthmatic; demanding renal; osteopathic; anti-organical; renal; osteopathic; resoluri; orti-asthmatic; demandic anti-infertility; ophthalmological; hepatitis; anorexia; decheral; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutein.

Homo sapiens. Synthetic.

/label- Phe, Leu, Val, ile, Ala, Tyr Misc-difference 227

WO200168859-A2.

COL SER 2000 CARD

15-MAR-2001, 2001WO-US08678.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing diagnosing and treating e.g. leukemia, asthma, diabetes; psoriasis; and glaucoma:

Claim 19; Page -; 158pp; English:

The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunoadulatory, anti-inflammatcory, anti-diabetic, anti-informal
have immunoadulatory, anti-inflammatcory, anti-diabetic, anti-inferrobial,
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascullar, cytostatic, anti-leukemic, anti-infertility and
optibalmological activities: The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
conclude, for example immune disorders (e.g. inflammation, diabetes and
colude, for example immune disorders (e.g. inflammation, diabetes and
transplant rejection), infections (e.g. hepatitis and septicaemia),
weight disorders (e.g. anorexis, cachesis and obseity), neuronal
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
con diseases (e.g. cystic fibrosis, asthma and emplysema), skin disease
(e.g. eczema and psoriasis), kindey disease (e.g. elumerulonephititis),
bone diseases (e.g. cystic fibrosis, asthma and emplysema),
con diseases (e.g. orsteoporosis and hypercalcaemia), vascular disorders
(e.g. stroke and atheroscierosis, cancers (e.g. lufertility and
miscarriage), eye disorders (e.g. qiaucoma and retinal neuropathy). The
construction recently also used as dispansite probes to detect and
construction and processing and hypercalcaemia) and dentify
construction and processing and processing and dentify may also be used as

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ö antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-Tibl7xlp:antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the Numan interleukin IT (IL-IT) receptor like protein sequence (AAU09904) and has been created according to information given inclaim 19:-0; Gaps ODFCGCEVALDLMEDFSLCREGOREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 120 121. RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFJAVFPDYSCEGDVPGILDLSTKFRLM 180 1 RKKQQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCESSKDGQNHMNVVQCFAYFL 60 statistic 199.6%; Score 2201; DB 22; Length 738; Similarity 99.8%; Pred. No. 1.4e-209; 1; Indels .0; Mismatches 416; Conservative 738 AA; antigens in Sequence Query Match Local Matches 19

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DNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE 240 241 KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300 SQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSG1YDSSVPSSELSLPLMEG 360 361 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSTTDELHAVAP 417 181 a õ 윱 õ 8 à ö 용

AAU09953 standard; Protein; 738 AA. AAU09953; RESULT

14-FREZUEZ (First entry)

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-diabetic; immunowodulatory; anti-diabetic; immunowodupressive; anti-nicrobial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukasmic; anti-infertility; ophthalmological; hepatitis; anorexia; cachaxia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; Human Interleukin 17 (hiL-17) receptor like protein substitution #3 nutein.

Homo saplens. Synthetic.

Location/Qualifiers 363 Misc-difference

WO200168859-A2

20-SEP-2001.

15-WAR-2001; 2001WO-US08678.
16-WAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460.
(AMGE-) AMGEN'INC.

(AMGE-) AMGEN INC.

WPI; 2001-611392/70. Jing S:

acids encoding interleukin 17 receptor like polypeptides, to preventing, disponsing and treating e.g. leukemia, asthma, psoriasis and glaucoma. useful for preventing, diagnosing a diabetes, psoriasis and glaucoma Nucleic

Claim 20; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunosuppressive, hepatic, anabolic, anotheractic, anti-alzebener's, remainmosuppressive, hepatic, anabolic, anotheractic, anti-alzebener's, remainmosuppressive, hepatic, anabolic, anotheractic, dernatological, on the properties of the properties of the statistic osteopathic, vascular cytostatic inti-leukaenic; anti-alzebener's, remainmosuppressive, anti-convulant, anti-convulant tractific and conversed and converse and atherosolerosis, andered as disquested and conversed and converse and atherosolerosis, cancers (e.g. lung disorders (e.g. conversed and conversed and conversed and conversed and converse and atherosolerosis, cancers (e.g. lung disorders (e.g. stroke and atherosolerosis, cancers (e.g. lung conversed and conver Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 20. expression and activity.

Sequence 738 AA;

Query Match
Best Local Similarity 99.5%; Pred. No. 3.4e-209;
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps

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441 61 ODFCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGNKYFVDKKNYKHKGGG 셤 ð

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KQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300 241 562 õ

0.750

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301 SOHGGIDODGEARPALDGSAALQPLIHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG 360
                                     LSTDOPETSSITESVSSSSGIGEEPPALPSKILSSGSCKADIGCRSTDELAAVAP 417.
        622
                                      361
                                                         682
                                       85 B
                  음
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RESULT 11

954 AAU09954 standard; Protein; 738 AA.

. AAU09954;

14-FEB-2002 (first entry)

interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-dobetic; immunosuppressive; anti-atcrobial; hepatic; anabolic; anti-definer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; ivasquiar; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexis; accheais, neuronal; dysfunction; lung:disease; bone, disease; vascular; eye disorder; cancer; human; mutant; Human Interleukin 17 (hIL-17) receptor like protein substitution #4.

Homo sapiens.

mutein.

Synthetic.

/label- Val, Ile, Met, Leu, Phe, Ala, Nie. Location/Qualifiers Misc-difference 37

W0200168859-A2

SPECIAL CONTRACTOR

15-MAR-2001; 2001WO-US08678.

16-MAR, 2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) , AMGEN INC.

Jing S;

WPI; 2001-611392/70.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma

Claim 21; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. Those receptor like polypeptides useful as vaccines and in gene therapy. Those have immunomodulatory, anti-inflammatory, anti-diabetic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, costeopathic, vascular, cytostatic, anti-leukemic, anti-infertility and optibal mological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These include, for example immune disorders (e.g. inflammation, diabetes and remappath rejection) infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cacheais and obesity), neuronal cystuction (e.g. Alzheimer's disease, parkinson's disease and epilepsy), uny disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. ecrema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and

breast cancer), reproductive disorders (e.g. Infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as disquistic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The ILI7rip may also be used as mitigans in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-ILI7rip antibodies and antagonists may also be used to down regulate Note: This sequence is not given in the specification but is based on thuman interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 21. QDPCGCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 120 QDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQPIIVVCSKGKKYFVDKKNYKHKGGG 441 121 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180 DNIPQLCSHIHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFE 240 241 KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300 SQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG 360 . 1. RKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFL 60 361 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP"417 FHILLITITETHELITITETHELITETHE 682 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCKADLGCR<u>SY</u>TQELHAVAP. 739 Ouery Match :: 99.4%; Score 2196; DB 22; Length 738; Best Local Similarity 99.5%; Pred. No. 4.3e-209; Matches 415; Conservative 0; Mismatches 2; Indels 0 expression and activity. Sequence 738 AA; 382 143 622 88888888888888 ð a . ð ි <u>සි</u> . 염

RESULT 12

AAU09956 standard; Protein; 738 AA.

AAU09956;

CEEB-2002, (first entry)

Human Interleukin 17 (hIL-17) receptor like protein substitution #6

Interleukin 17; hil-17 receptor like protein; immunomodulatory; anti-diabelic; immunosuppressive; anti-diabelic; hepatic; anabolic; anci-diabelic; anti-alzheimer's; anti-parkinsonlan; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatilis; anorexia; cachexia; neuronal-dysfunction; ining disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutant;

Homo sapiens.

Synthetic

Location/Qualiflers Misc-difference 515

/label- Asp, Glu

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20-SEP-2001.
15-MAR-2001; 2001WO-US08678.
                  16-MAR-2000; 20000S-189816P.
28-NOV-2000; 20000S-0724460.
                                     WPI; 2001-611392/70.
                          (AMGE-) AMGEN INC.
  W0200168859-A2.
      20-SEP-2001.
                                Jing S;
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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunoadulatory, anti-inflammatory, anti-diabetic, anti-inferiolial,
immunosuppresslave, hepatic, anabolic, anti-diabetic, anti-inferiolial,
confedential activities The IL-17 receptor like nucleic acids and
proteins any be used to prevent and treat diseases associated with
proteins any be used to prevent and treat diseases associated with
proteins any be used to prevent and treat diseases associated with
confide, for example immune disorders (e.g. inflammation, diabetes and
tramplant rejection), infections (e.g. hepatitis and septicemia),
confide, for example immune disorders (e.g. inflammation, diabetes and
tramplant rejection), infections (e.g. hepatitis and septicemia),
confiders (e.g. oystic fibrosis, asthma and emphysema), skin disease
confiders (e.g. oystic fibrosis, asthma and emphysema), skin disease
(e.g. stroke and atherosolerosis and hypercalcaemia), vascular disorders
(e.g. stroke and atherosolerosis, cancers (e.g. infertility and
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
DNA and its complements may also used as insamples and dientify
patients needing restorative charapy. The ILI771p may also be used as
anys to identify modulators of anthodies against the proteins and antigens in the production of antigodies may also be used to down regulate
entreasion and archity modulators of expression and activity. The
antigens and archity entreasing and antagonists may also be used to down regulate
entreasion and archity entreasion and archity and
antigens and menta and antagonists may also be used to down regulate on the expression and activity.

Note: This sequence is not given in the specification but is based on thuman interleukin 17 (IL-17) receptor like protein sequence (AAN09904) and has been created according to information given in claim 23. Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis, and glaucomay. Claim 23; Page ..; 158pp; English. expression and activity.

Sequence 738 AA;

ö 1 RKKQGENIYSHLDBESSESSTYTAALPRERLRPRPKVFLCISSKDGQNHMNVVQCFAYFL 60 ö Query Match 99.3%; Score 2194; DB 22; Length 738; Best Local Similarity 99.5%; Pred. No. 6.8e-209; Matches 415; Conservative 0; Mismatches 2; Indels 0; Query Match Best Local Similarity <u>유</u>. 8 ð

121 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVTFDYSCEGDVPGILDLSTKYRLM 180

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AAU09955 standard; Protein; 738 AA. .13....

14-FEB-2002 (first entry)

Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory auti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; hepatitis; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachazia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; Buman Interleukin 17 (hIL-17) receptor like protein substitution #5. mutein.

Homo sapiens. Synthetic.

/label* Cys, Ser, Ala Location/Qualifiers Misc-difference 385

WO200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US08678.

16-MAR-2000; 2000US-189816P. 28-NOV-2000; 2000US-0724460.

(AMGE-) AMGEN INC

Jing S;

WPI; 2001-611392/70.

receptor like polypeptides, treating, e.g. leukemia, asthma, Nucleic acids encoding interleukin 17 useful for preventing, diagnosing and diabetes, psoriasis and glaucoma

Claim 22; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomialitory, anti-inflamentory, anti-idabetic, anti-inforbial, anti-parkinsonian, anti-copial, anti-parkinsonian, anti-copial, anti-parkinsonian, anti-copyulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukamic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL) associated with include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal NAME OF STATE OF STAT

Synthetic.

888888888888888888

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lung-disorders (e.g. cystic fibrosis, asthma and emphysems), skin disease (e.g. cystic fibrosis, asthma and emphysems), skin disease (e.g. cystic fibrosis, and hypercalcemans), vascular disorders (e.g. glomerulonephritis), bone diseases. (e.g. cysteoporosis and hypercalcemans), vascular disorders (e.g. intertility and constraints), reproductive disorders (e.g. infertility and complements (e.g. diaucoma and retinal neuropathy). The DNA, and its complements may also used as disquostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify antiques needing restorative therapy. The Inlitin may also be used as intigens in the production of antibodies against the proteins and in assays to identify modulators (expression and activity, where the antibodies and antagonists may also be used to down regulate
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and activity.

Whose: This sequence is not given in the specification but is based on thuman interleukin 17 (11-17) receptor like protein sequence (AMU09904) and has been greated according to information given in claim 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ODFCGCEVALDLWEDFSLCREGOREWVIOKIHESOFIIVVCSKGMKYFVDKKNYKHKGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLAMEG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 RKKQQENITSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGONHWNVVQCPAYFL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSTDQTETSELTESVSSSSGLGEEEPPALPSKLLSSGSCKADLGCRSYTDELHAVAP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 DNIPOLCSHIHSRDHGLOEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHOFIDEEPDWFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match... 99.1%; Score 2190; DB 22; Length 738; Best Local Similarity 99.5%; Pred. No. 1.7e-208; Matches 415; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 AA;
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Interleukin 17; hIL-17 receptor like protein; immunomodulatory; anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Interleukin 17 (hiL-17) receptor like protein substitution #7
AAU09957 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002 (first entry)
                                                                                                                                                                                                  AAU09957;
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Homo sapiens.

64 CA 18

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The invention describes novel nucleic acids encoding interleukin (IL) 17
receptor like polypeptides useful as vaccines and in gene therapy. These
receptor like polypeptides useful as vaccines and in gene therapy. These
have immunosuppressive, hepatic, anabolic, anti-diabetic, anti-alzheimer's, renal,
that in the polypeptide anti-convulsant, anti-asthmatic, dermatological,
costeopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
optibalmological activities. The IL-17 receptor like nucleic acids and
proteins may be used to prevent and treat diseases associated with
proteins may be used to prevent and treat diseases associated with
contains may be used to prevent and treat diseases associated with
propriate IL-17 receptor like polypeptide (IL)Thip) expression. These
include, for example immune disorders (e.g. infilammation, diabetes and
transplant rejection), infections (e.g. infilammation, diabetes and
cransplant rejection), infections (e.g. infilammation), altherance
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
cone diseases (e.g. cystic fibrosis, asthma and emphysemal, skin disease
(e.g. eczema and psoriasis), kindery disease (e.g. glomerulonephritis),
bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
(e.g. stroke and atherosolerosis, cancers (e.g. infertility and
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
Drast cancer), reproductive disorders (e.g. infertility and
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
Drast cancery, reproductive disorders (e.g. infertility and
antiques in the production of antipoles against the proteins and in
antiques in the production of antipoles against the proteins and in
assays to identify modulators of similar mucleic acids in samples and identify
antiques. In the production of attended as dispans the proteins and in
antiques. In the production of attended assays to identify modulators of expression and activity. The
antiques in apple and and apple and activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and activity. Note: This specification but is based on the Note: This sequence is not given in the pecification but is based on the human Interleukin 17 (IL-17); receptor like protein sequence (AAU09904) and has been created according to information given in claim 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding interleukin 17 receptor 11ke polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 120
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                                                                                        /label- Cys, Ala, Ser
                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page -; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes, psoriasis and glaucoma
                                                                                                                                                                                                                                  15-MAR-2001; 2001WO-US08678.
                                                                                                                                                                                                                                                                                 16-MAR-2000; 2000US-189816P.
28-NOV-2000; 2000US-0724460
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Matches . 415; Conserva
                                                                   Misc-difference 60
                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                          WO200168859-A2.
                                                                                                                                                                                      20-SEP-2001
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181 DNI.POLCSHLASRDHGLOEPGGHTROGSRRNYFRSKSGRSLYVAICHMHQFIDEEPDWFE 240
                                      442 RGSGRGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYEDYSCEGDVPGILDLSTKYRLM 501
                                                                         KOFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 300
                                                                                       361 LSTDQTETSSLTESVSSSGLGEEEPPALPSKLLSSGSCK#DLGCRSYTDELHAVAP 417
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ABB07630 standard; Protein; 739 AA. RESULT 15

ABB07630;

GOTANT TOUZE (Hirst entry)

Murine cytokine receptor, 2cytor18.

Cytokine receptor; Zcytori8; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumour; erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

Mus sp.

W0200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US23253.

26-JUL-2000; 2000US-220747P

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE,

WPI; 2002-217048/27. N-PSDB; ABA95037, ABA95038.

New cytokine receptor polypeptide designated zcytori8, useful for inhibiting cell proliferation associated with psoriasis or tumor growth, and modulating immune system by binding to endogenous zcytori8 ligand.

Claim 1; Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytoris. The Zcytoris polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytoris in vivo by gene therapy techniques. Zcytoris oligonucleotide probes are useful for in vivo disponsis, and the Zcytoris probes and primars can be used to detect and localize Zcytoris gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytoris gene resides. The Zcytoris polypucicotides can also be used in linkage-based testing of pulmonary, alveolar proteinosis, familial periodic fever and erythrolukemia, and erythroleukemia associated with murins zone of cytokine receptors. The present sequence represents a murins zone. murine Zcytor18 amino acid sequence

560 EKQPIPEQHPPVRYQEPVLEKFDSGLVLNDVISKPGPESDFCRKVZACVLGAAGPADSIS 619 503 DELPELCATION - GROEVICQHPGESRRYFRSKSGRSLYVAICHMEDEEDDWF 559 240 EKQEVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQH 299 443 RGEAGGEFTVAVAAIAEKIRQAKQSSSAAIRKFIAVFFDYSCEGDVPCSLDISTKKIM 502 181 DNLPQLCSHLHSRDHGLQEP-GQHTRQGSRRNIFRSKSGRSLIVAICNMHQFIDEEPDWF 239 300 --ESONGGIDODGEARPALDGSAALQPILLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPL 357 Db --- 5323 REKQQENIYSHLDEESPESSTVAAALPRDRLRPQPKVFLCTSNKDGQNHGNVVQCFAYFL 382 * 61 ODFCGCEVALDLWEDFSLCREGOREWIOKIHESOFIIVVCSKGMKYFYDKKNYKHKGG 120 121 RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLM 180 9 7; Gaps 620 YLESQHYGLDQDTEAQPSCDSAPALQPLHAVKAGSPSENPRDSGIIDSSYPSSELSLPL 1 RKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAFFL 418 L 418 " 739 δ õ ð à ò 셤 à - 유 ð ä ö 셤

rch completed: May 19, 2003, 09:20:02 time: : 32.4416 secs Search Job tim

Sequence

34 88 4.0 12364 1 PGCA_BOVIN	ALIGNMENTS		GN ILL17R. OS HOMO Sapiens (Human). OC RUKARYOCLA; Mcrazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. OX NCBL_TAXID-9606;	RV [1] RC TISSUE-T-cell; RX MEDLINE-9803563; PubMed-9367539; RA Tao E. "Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S., RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.; RY receptor."; RY receptor."; RY receptor."; RY Cytokine 9:794-800(1997).	\$	C This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the Buropean Bioinformatics Institute. There are no restrictions on its C use by non-profit institutions as long as its content is in no way co modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch). CC PREME, 189917, AMB99791.1:	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	and actions and						
n 5.1.4_p5.4578. Compugen Ltd. arch time 8.48731 Seconds (without alignments) 2042.709 Million cell updates/sec	CKADLGCRSYIDELHAVAPL 418	112892		is the number of results predicted by chance to have a liter than or equal to the score of the result being printed, lived by analysis of the total score distribution SUMMARIES Query Match Length DB ID Description	096646 homo sapten 060943 mus musculu 090rm6 homo sapten 010138 ceenorhabdi 091493 mus musculu 060821 mus musculu 060821 mus musculu 004996 arabidopsis 004996 arabidopsis	009194 Mutrhe cyto 004982 gallus gall 934908 coturnix co 06421 mus musculu 998154 mus musculu 998154 mus musculu 09ere9 mus musculu 02799 sus serofa 061361 mus musculu 970771 caenorhabdi	
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                                                                                                                                                                            Gaps 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel cytokine receptor.";
Immunity 3:811-821(1995).
-1- FUNCITON: Receptor for IL17. Binds its ligand with low affinity,
suggesting that additional components are involved in IL17-induced
                                                                                                                                                                                                                                        1: 1: 1 | 1 | 1 | 1 | 1 | 1 | 353 EKYSDDTKTTDGLEVADLIPPPLKPRKVWIIYSA-DHPLIYDVVKKRAQFLLTACGTEVA 411
                                                                                                                                                                                                                                                                                                                                                      --- RGSGKGELFLVAVSAIAEKLRQAKOSSSAALSKFIAVYF-DYSCEGDVPGILDLSTK 176
                                                                                                                                                                                                                                                                         IDLWEDFSICREGOREWV----IQKIHESQPIIVVCSKGMKYFVDKKNYKHKGGG-----120
                                                                                                                                                                                                                                                                                                                                                                                 468 RCDEGKPVGDLFTAAMMILDPFKR----PACFGTYVVCTFSEVSCDGDVPDLFGAAPR 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 EPDWFE-----KQFVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 AVLGATGPADSQHE----ALQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638 LYGEEGGAAVAKLEPHLOPRGOPAPOPLHTLYLAAEEGALVAAVEPGPLADGAAVRLALA 697
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                                                                                                                                                                                                                    14 RESSESSITITAALPRERIRPRP ---- KVFICYSSKDGONHMNVQCFAYFLQDFCGCEVA 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signaling (By similarity).

-I. SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
                                                                                                                                        ; f . .
13.00
                                                                .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                  (POTENTIAL).
                                                                                                                                              13.9%; Score 308; DB 1; Length 866; 28.3%; Pred. No. 1.9e-15; ive 60; Mismatches 173; Indels 88;
                                                                                                                         ¥.
                      225 N-LINKED (GLCNAC. . .) (POT 242 N-LINKED (GLCNAC. . .) (POT 265 N-LINKED (GLCNAC. . .) (POT 267 N-LINKED (GLCNAC. . .) (POT 267 N-LINKED (GLN REF. 1).

S80 (H ->- R (LIN REF. 1).
96131 MW; 28330BED2303B0C9 CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-17 receptor precursor (IL-17 receptor).
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7060943;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                Best Local Similarity 28.39 Matches 127; Conservative
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MEDLINE-96111968; PubMed
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866 AA;
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the Buropean Bioinformatics Institute. There are no restrictions on its use why non-profit sinstitutions as long as its content is in no way modified and this statement is now, removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 IDELERGYISEVGYMYWYSRQKQEMYESNSKIIILGSRG----TQAKWKALLGWAEPAY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYPLADRPEEV--YFRIQDLEMFEPGRAHHVRELTGONYLQSPSGRQLAEAVLREQEWQ 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233. DEEPDWFEKQFVPFHP----PPLR-..-YREPVLEKFDSGLVLNDVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 TVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL------MEGLSTDQT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 AAVIGATGPADSQHESQHGGLDQD--------GEARPALDGSAALQPLLH 327
                                                                                                                                                                                                                                                                                                                                                                            14 EESSESSITITAALPRERLRPRP----KVFLCYSSKDGONHMNVQCFAYFLQDFCGCEVA 69
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 417 Last annotation update)
Interleukin-17a receptor precursor (IL-17B receptor) (IL-1
homolog 1) (IL-17Rhi) (IL17Rhi) (Cytokine receptor (RL4).
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                                                                                                                                                                             *: "EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;
                                                                                                                                                                                                      CYTOPLASMIC . (POTENTIAL) .
                                                                                                                                                            INTERLEUKIN-17 RECEPTOR
                                                                                                                               Receptor, Transmembrane, Signal, Glycoprotein, SIGNAL, 1 . . . . . . POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT 105 502 AA.
                                                                                                                                                                                            POTENTIAL.
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                                                                                       EMBL; U31993; AAC52357.1;
                                                                                                                                                                                                                                                                                                                                                                                             Matches 120; Conservative
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Q9NRM6; Q9BPZ0; Q9NRL4; C
                                                                                                                  MGD; MGI:107399; Ill7
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                                                                                                                                              SIGNAL
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82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 AEL 479
              CARBOHYDVS: 156
CARBOHYD 183
                                            CARBOHYD 1 CARBOHYD 2 VARSPLIC 2
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Q10128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. Biol. Chem. 276:1660-1664(2001).

1. FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. Way play a role in controlling the growth and/or differenciation of hematopoletic cells.

1. SUBCELLUIAR LOCATION: Type I membrane protein (isoform 1);

8 EGTORED (isoform 2).

1. ALTERNATIVE PRODUCES: 2 isoforms; 1 (shown here), and 2; are produced by alternative splicing.

1. TISSUE SPECIFICIATY: Expressed in several endocrine tissues, mostly in fetal and adult liver, kidney, pancreas, testis, colon, brain and small intestine; not detected in peripheral blood leukocytes, lymphold organs, and most cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Tansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.; "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17Rhl.";
                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-20273223; PubMed-10815801;
Tian E., Sawyer T. T.R. Largaespada D.A., Jenkins N.A., Copeland N.G.,
Shaughiessy J.D. Jr.,
"Evi27 encodes a novel membrane protein with homology to the IL17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing. SIGNAL
                                                                                                                                                                                                                                                                 TISSUE-Lung;

WEDLINE-2017118; PubMed-10749887;
Shi Y. Shi X. Shang J., Connolly K., Wizzegorzewski K.J.,
Shi X., King W., Wathen K.; Hodge V., Fisher C.L., Olsen H.,
Barber M.C., Wang W., Wathen K.; Hodge V., Wilkinson K.A.,
Carrell J.A., Ebner W.

A novel cytokine receptor-ligand pair. Identification, molecular
characterization, and in vivo immunomodulatory activity.";
J. Biol. Chem., 275:19167-19176(2000).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
Zhang W., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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MIM; 605458; -.
                                                                                                                                                                                            Oncogene 19:2098-2109(2000).
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CARBOHYD
CARBOHYD
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183 ... 156 ... 156 ... N-LINKED (GLCNAC....) (POTENTIAL).
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Rhabditidae; Peloderinae; Caenorhabditis.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 81.6 KDm protein F56D1:2 in chromosome II precursor.
F56D1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 127.5; DB 1; Length 502; Best Local Similarity 24.6%; Pred. No. 0.03; Matches 45; Conservative 31; Mismatches 92; Indels 15;
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HYPOTHETICAL PROTEIN F56D1.2.
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                                                                                                                                                                                                                                                                                                                                                                                                       289 502 "" MISSING (IN ISOFORM 2).
6 6 6 L -> I (IN REF. 1).
422 426 LEPLA -> SSPCL (IN REF. 2).
427 502 MISSING (IN REF. 2).
468 2468 L -> F (IN REF. 1).
502 AA; 55884 WW; CDB87586FARE49CC.CRC64;
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718 AA; 81622 NW; 4289E056288417AA CRC64;
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WormPep; F56D1.2; CE01970.
Hypothetical protein; Transmem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANBOUS: EV127 is a common site of retroviral integration in BRHZ murine myeloid leukemias, localized near the ILL/BR gene. Proviral integrations result in increased expression of ILL/BR on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted (1soform 2).

**ALTERNATIVE PRODUCTS: 2 lsoforms; 1 (shown here) and 2; are produced by alternative splicing.

**TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid
                                                                                                                                                                                                                                                                                                                                                                                       516 --IRDATHREPEARKKIAVVRFNYS--PHVPPNLAILNLPT-FILPEQFAQLAFLHNVE 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 H TERANVIQUISEAQIHEMNICASRUMSFEVRNENMLETRWRENDELAA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 IDODGEARPALDGSAALQPILHTVKAGSPSDM--PROSGITDSSVPSSELSLPLMEGLST 363
                                                                                  398 RDKVRSREVRUIALTEFVKVMIVYAD-DNDLHTDCVKKLVENLRNCASCDPVFDLEKLIT 456
                                                                                                                                                                                                                                                       457, AEQIVPSRWLVDQISSLKKFIIVVSDCAEKILDTEASETHQLVQARPFADLFGPANEMI- 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 HGLQEPGQHTRQGSRRNYFRSKSGRSLY---VALCNMHQFIDEEPDWFEKQFVP----- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246, FHPPPLRYREPVLEKFDSGLVLNDVNCKPGPESDFCLKVEAAVLGATGPADSQHESQHGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 LH--LKRQSPVIVPIQT------EED---RIAASIKINLVPPQALVDSD--- 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             658 - DED------DYDLQP--HASHQNQPLILLPPEQCG-----PDSD-----SD 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09JI3; 09JIP2;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-17B receptor precursor (IL-17B receptor)
homolog 1) (IL-17Rhl) (IL17Rhl) (IL-17ER).
                                                                                                                                                                    78 LCREGORENVIORIHESQFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIA 137
                                                                                                                                                                                                                                                                                                                                     136 EKLROAKOSSSAALSKFIAVYFDYSCEGDVP---GILDLSTKYRLMDNLPQLCSHLHSRD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-20273223; Pubmed-10815801;
Tada E., Savyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,
Shaughnessy J.D. Jr.;
"Evi27 encodes a novel membrane protein with homology to the IL17
28 RERIAPRP-----KVFLCTSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacopone 19:2098-2109(2000).
-I-FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17F. May play a role in controlling the growth and/or differenciation of hematopoleito cells.
-I- SUBCELLULAR LOCATION: Type I membrane protein (180form 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             691 SESDSSSESESEDNEG---EDPKTIVVK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 DOTETSSLIESVSSSSGLGEEEPPALPSK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LI7BR OR EVI27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7S_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor.
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F 0 - 2 0 - 1

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SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Brain;
STRAIN-BALB/C; TISSUE-Brain;
STRAIN-BALB/C; TISSUE-Brain;
STRAIN-BALB/C; TISSUE-Brain;
Gengyo-Ando K., Kitzyama H., Mukaida M., Ikawa I;;
Gengyo-Ando K., Kitzyama H., Mukaida M., Ikawa I;;
Gengyo-Ando K., Kitzyama H., Mukaida M., Ikawa I;;
Gengyo-Ando K., Kitzyama H., Mukaida H., Ikawa I;;
Gengyo-Ando K., Kitzyama H., Mukaida H., Ikawa I;;
J., Neurosci. 16:6695-6702(1996)
J., Neurosci. 16:6695-6702(1996)
J., Neurosci. 16:6695-6702(1996)
J., Shailarii: BELONGS TO THE STRBP/UNC-16/SECI PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...) (POTENTIAL).
HINYMAX KACOTEAGEMADPITACKRINEWYEVYEVENTUPLIA.
GINEYTILOGEOTILG ->. TRENTEYTSGYFPAAKHOALRI
SAPFELGFPRGPEDSVILPPQPLASLFHDEVKLT (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 REGOREWVIOKIBESOFIIVVCSKGMKYFVDKKNYKHKGGGRGSGKGELFLVAVSAIAEK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 ENGPVONITTORGAADKVVFLLPSDVPTLCDSACGHNEGSARENSQ-DLFPLAFNLFCSD 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 STYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-TBC) (RUNC-18-3).
SYXRP3 OR UNC18C.
                                                                                           keceptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tellam J.T., McIntosh S., James D.E.; "Molecular identification of two novel Munc-18 isoforms expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                 CTTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ; (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.0%; Score 110.5; DB 1; Length 499; Best Local Similarity 24.1%; Pred. No. 0.55; Matches 3.40; Conservative 27; Mismatches 82; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 LRQAKOSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 F----SSQTHLHKYLVVYL-----GGADLKGDYNALSVCPQ 462
                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          ASSING (IN ISOFORM 2).
C66440430E3C31F3 CRC64;
                                                                                                                              INTERLEUKIN-17B RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 A.A.
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    ISOFORM 2)
                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-neuronal tissues.";
J. Biol. Chem. 270:5857-5863(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-95197608; Pubmed-7890715;
                        EMBL; AF208109; AAF86049.1; -. EMBL; AF208109; AAF86050.1; -.
                                                                                                                                                                                                                                                                                                                                              219 499 M
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                                                                       GD; MGI:1355292; Ill7br
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Q60770;
                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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SEQUENCE
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                            CARBOHYD
                                                                                                                              CHAIN
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794 AA;
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CONFLICT
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Best Local
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                                                                                                                                                                                                                                           Query Match

4.84; Score 105.5; DB 1; Length 592;
Best Local Similarity 18.84; Pred. No. 1.6; B
Matches 89; Conservative 60; Mismatches 145; Indels, 179; Gaps 21;
                                      was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send, an email to licenselsb-sib.ch).
                                                                                                                                                                                                                                                                                                            6 RNIYSHLDEESSESSTYTAALPRERLRPRPKVFLCTSSKDGQNHMNVVQCFAYFLQDFC- 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1551_MOUSE STANDARD; PRT; 794 AA.
050021; 050059;
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
21nc finger protein 151 (Polyomavirus late initiator promoter binding protein) (LP-1) (Zinc finger protein zi3).
ENFISI OR ZFPI00.
                                                                                                                                                                                                                                                                                                                                              63 ENIKRNREPVROMKALYE-----ISPTPKSVDCFLRDFGSKSEKKYKAAYIYFTDFCP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                90 KIHESQPIIVVC-----SKGMKY------FVDKK---NYK--HKGGGRGSGKG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 DSLFHKIKASCSKSIRRCKEINISFIPQESQVYTLDVPDAFYYCYSPDPSNASRKEVVME 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127. ELFLY-----AVSAIAEKLROAKOSSSAALSKFIAVYFD-----YSCEG-DVPGI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 L----DLSTKYR-----LMDNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 AEGORVKDSMLVLLPVLL--NKNHDNCDKIRAVLLYIFGINGTTEEN------ 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 SLSALTQLMKKMPHFRKQISKQVV----HLNLAEDCMNKFKLNIEKLCKTEQDLALGTD 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 -----DSGLVLNDVMCRPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARP 314
                                                                                                                                                                                                                                                                                                                                                                                     Nus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 ALDGSAALQPILLHTVKAGSPSDMPRD-SGIYDSSVPSSELSLPLMEGLSTDQT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rapp L., Carmichael G.G.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       592. AA; 67942. MW; 7874B71DE107871A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CBA; TISSUE-Kidney;
MEDLINE-96003919; PubMed-7575457;
Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;
                                                                                                                     EMBL; U19521; AAA69913.1; -...
                                                                                                                                                      MGD; MGI:107362; Strbp3.
LiterPoor; TR001619; Seci-like.
Pfam; PF0095; Seci; 1.
Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       SEQUENCE
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                                                     64 CGCEVALDLWEDFSLCREGOREWVIOKIHESQFIIVVCSKGMK-YFVDKKNYKHKGGGRG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGKGELFLVAVSAIAEKLRQAKOSSS-----AALSKFIAVYFDYSCEGDVPGILDLST 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 KYRLADNLPQLCSHL-HSRDHGLQEPGQH-----TRQGSRRNYFRSKSGRSLY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 ACHTLKSLAEPSSTTGESADASAVEGGDKRAKDERAAATMLSRLGQARGSSSTGPGRELK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 VAIÇINHAQFIDEEPDWFEKQFVPFHPPPLRIREPVLEKFDSGLVLADVMCKPGPESDFCL 282
                                                                                                                                                  -1- SUBCELLUIAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 CDCTFVVD-GVDF------KAHKA--VLAACSETFKALFVDQKDVVHLDISNA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS50097; BTB; 1.
PROSITE; PS00026; ZINC_FINGER_C2H2_1; 13.
PROSITE; PS01075; ZINC_FINGER_C2H2_2; 13.
TRANSCTIPTION FG9ULALION; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                      -1. SIMILARITY: BELONGS TO THE RRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS...
"An unusual arrangement of 13 zinc fingers in the vertebrate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5%; Score 99.5; DB 1; Length 794; 20.6%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --> A (IN REF. 2).
-> K (IN REF. 2).
FFF88E56EDEBF7ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE
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InterPro; IPR000822; Enf_C2H2.
Pfam; PF00096; zf_C2H2; 13.
Pfam; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD0000003; Znf_C2H2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U22396; AAA64848.1; -.
EMBL; U14556; AAA85493.1; -.
HSSP; PO8046; 1A1H.
MGD; MGI:107410; Zfp100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0048; ZINCFINGER
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                                                                                               207 AARARALSESSEQEMEVEPASKG--EDGQEEEGAGPATVKEEGMH-LDNGEPPEENEESA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nurine leukemia virus o
Retroid viruses; Retroviridae; Mammalian type C retroviruses
283 KVEAAVLGATGPADSQHESQHGGIDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRDSG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83221648; PubMed-6304726;
Reddy E.P., Smith M.J., Srinivasan A.;
Nucleotide sequence of Abelson murine leukemla virus genome:
structural similarity of its transforming gene product to othe
gene products with tyrosine-specific kinase activity.";
Proc. Natl. Acad. Sci. U.S.A. 80:3523-3627(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tyrosine phosphate.
                                                                                                                                                             343 IYDSSVPSSELSLP---LMEGLSTDQTETSSLTESVSSSSGLGEE 384
                                                                                                                                                                                                         264 GTDS---GOELGMEGONLRSGIYGDRIESKAYGSIIHKCEDCGKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reddy E.P., Smith M.J., Srinivasan A.;
Proc. Natl. Acad. Sci. U.S.A. 80:7372-7372(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase transforming protein ABL
                                                                                                                                                                                                                                                                                                      746 AA. 🗗
                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILI.,
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; VO1541; -; NOT_ANNOTATED_CDS.
EMBL; K00010; AAA46470.1; -.
FIR; A00627; TVMVGM.
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InterPro; IPR000980; SH2.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abelson murine leukemia virus ()
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 588-746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCB1_TaxID-11788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              ABL_MLVAB ST.
P00521;
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21-JUL-1986 (
15-JUN-2002 (
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                                                                                                                                                                                                                                                                                                                                                         181 HPMLVQLIGYCTREPPFYIITEFMTGNLLD-----YLRECNRQEVSAVV--LIMMATQ 232
                                                                                                                                                                                                                                                                                                                                                                                                               101 CSKGMKTFVDKKNYKHKG-GGRGSGKGELFLVAVSAIA-EKLRQAKQSSSAALSKF---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- PGILDLSTKYRLMDNLPQLCSHLHS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 TAPESLAYNKESIKSDVWAFGVLAMEIATYGMSPYPGI-DLSQVYELLE------ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 OF-----POPERPPPLRYREPVLEKFDSGLVLNDVMCK----PGPESDFCLK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 VEAAVLGATG --- PADSQ ----- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 DGSAALQPILHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 HMNVVQCFA-----YFLQDFCGCEVALDLWEDFSLCREGOREWVLQKIHESQFIVV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 ISSAMEY-LEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTTTAHAGAKFPIKW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 KDIRMERP----BGCPERVYELMRACWQWNPSDRPSFAEIHQAFETWFQESSISDEVER 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 ELGKRGTRGGAGSMLQAPELPTKTRTCRRAAEQKASPPSLTPKLLRRQVTASPSGLSHK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 KEATKGSASGMCTPATAEPAPPSNKVGLSKASSEEMRVRRHKHSSESPGRD---KGRLAK 511
                                                                                                                                                                                                                                                                                  Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 RDHGLQEPGQHTRQGSRRNYFR-----SKSGRSLYVAICNMHQFIDEE---PDWFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant J. 4.137-150(1993).

-1- FUNCTION: BINDS ONLY TO LARGE DNA FRAGMENTS. RECOGNIZES A DNA FRAGMENT CARRIING 8 COPIES OF BOX7 MOTIF OF THE LIGHT-INDUCED CAB-E PROMOTER OF NICOTIANA PLUMBAGINIFOLIA. ALSO RECOGNIZES THE BOX7MI MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schindler U./ Beckmann H. Cashmore A.R.;
#RATS 1. a novel Arabidopsis homeodomain protein containing a
                                                                                           Polyprotein; Tyrosine-protein kimase; Transferase; Oncogene; SH2 domain;
                                                                                                                                                                                                                                    DB 1; Length 746;
                                                                                                                                                                128 379 3 M. PROTEIN KINASE: 7 46 AA; 81872 MW; B9072FFF55FE9257 CRC64;
                                                                                                                                                                                                                                                      Best Local Similarity 20.7%; Pred. No. 10;
Matches 90; Conservative 52; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN:2002 (Rel. 41, Last annotation update)
PROSITE; PSO0107; PROTEIN KINASE_ATP; 1.
PROSITE; PSO0109; PROTEIN KINASE_TRR; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 AA.
                                                                                                                                                                                                                                  4.4%; Score 96.5; 20.7%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 ----IAVYPDYSCEGDV-----IAVYPDYSCEGDV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-94035169, PubMed-8106082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox protein HAT3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 SSSCLGEEEPPALP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 ---GLRKPVPPSVP 579
                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HT31_ARATH
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                       Query Match
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HT31_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 KCGSKDLSVDNDIILCDGFCDRGFHQYCLEPP--LRKEDIP--PDDEGWLCPGCDCKDDS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 KSG-RSLYV --- - AICN --- - - MHQFIDEEPDWFEKQFVPFHPPPLRYREPVLE-KFDS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 QHGGLDQDGEARPALDGS------AALQPLLHTVKAGS------PSDMPRDSGIYD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 DEDGSD-DNEESENEDGSSDETEPTSASDEMIESFKEGKDIMKDVMALPSDDSEDDD-YD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 SSVPSSELSLPLMEGLSTDQTETSSLTESYSSSGLGE-----EEPPALPSKLLS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 KGMKYFVDKKNYKHK-----GGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ::||::: ||: |
120 KKLRYFLNRINYEQSLIDAYSLEGWKGSS--------EKIRPEKELERATKE--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 AVYFDYSCEGDVPGILDLSTKYRLADNLPQLCSHLHSRDHGLQEPGQHTRQGSRRNYFRS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 -----ILRASIKIDIFOHIDTICARGSIPESIFOTOGEI----SSEDIFCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 GLVILNDVMCKPGPESDFCLKV····EAAVIGATGPAD------SQHES 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 4.3%; Score 96; DB 1; Length 660; Local Similarity 21.4%; Pred. No. 9.4; Assatches 129; Indels 112; Gaps 189; Conservative 49; Mismatches 129; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00027; HOMEOBOX_1; 1.
PROSITE: PS0001; HOMEOBOX_2; 1.
PROSITE: PS010359; EE_PHD_1; 1.
PROSITE: PS50016; EE_PHD_2; 1.
HOMEODOX; DNA-binding; Nuclear protein; Transcription regulation;
- SUBCELLULAR LOCATION: Muclear ...
- TISSUE SPECIFICITY: PRIMARILY DETECTED IN ROOF TISSUE...
- SIMILARITY: SPECIFIC THE PROPERSOCIATED HOMEOBOX FAMILY...
- SIMILARITY: CONTAINS 1. PHD-TYPE INC.FINGER...
- SIMILARITY: CONTAINS 1. FROMEOBOX DOMAIN....
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551 610 HOMEOBOX.
660 AA; 73604 MW; A3B265CD394DA138 CRC64;
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                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR001965; Znf PHD.
Pfem; PF00046; Homeobox; 1.
Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                   EMBL; X69512; CAA49263.1;
HSSP; P41778; 1DU6.
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ZN_FING
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SEQUENCE
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Best Local 5
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PRGR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Atomic structure of progesterone complexed with its receptor.";
Nature 393:397:396 (1998).

-i-ruce 393:397:396 (1998).

-i-ruce 393:397:396 (1998).

THE REGULATION OF EURARYCTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION NO DIFFERENTIATION IN TARGET TISSUES.

-i-SUBCELLULAR LOCATION: NUCLEAR.

-i-SUBCELLULAR LOCATION: STORMAN AND B (SHOWN HERE); ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRODUCED BY ALTERNATYE SPLICING:
-1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR3 SUBPANILY:
                                                                                                                                                                                Chambon,P.; 110.110.11 a./v. interpretable of the chambon progesterone encoding the two functionally different human progesterone receptor
MEDILINE-87184565; PubMed-3551956; MEDILINE-87184565; PubMed-3551956; Loosfelt H., Merlel C., Misrahl M., Atger M.; O'Auriolill., Loosfelt H., Merlel C., Eridlansky F., Gulochon-Mantel: A., Gallbert F., Milgrom B.; Complete amino acid sequence of the human progesterone receptor deduced.from cloned.cDNA.;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Kieback D.G., Agoulnik I.U., Tong X.-W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY.CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933.
MEDLINE-98282128; Pubmed-9620806;
                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 143:740-748(1987).
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InterPro; IPR001628; Inf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000536; Hormone_rec_11g.
InterPro; IPR000128; Progest_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Znf_Cesterold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF02161; Prog_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00047; STROIDFINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X51730; CAA36018.1; -: EMBL; M15716; AAA60081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF016381; AAD01587.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams S.P., Sigler P.B.; Atomic structure of proges
                                                                                                                                                                                                                              forms A and B.";
EMBO-J::9:1603_1614(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; 100696; --
Genew; EGNC:8910; PGR.
NIM; 264080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1A28; 15-JUL-98
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
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13;

Gaps

DB 1; Length 841;

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192 SEDHGLØEPGQHTRØGSRR-----NYFRSKSGRSLYVALCNWH------ 229
                                                                                       Query Match

4.34;1°Score 94.5; DB 1; Length 8
Best Local Similarity; 8.23;4°p. Fred; No. 16;
Matches 58; Conservative 8.85; Mismatches 73; Indels
Transcription regulation.
SEQUENCE 1841 AA; -92706 MW; 9F18372739D723E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X67052; CAA47436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 SSG---SCKAD 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721 EEALEERCERD 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEURAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMIL_CHICK
Q04982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
RMIL_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORILATION BY CK).
PHOSPHORYLATION (BY CK).
MISSING (IN ISOPORM A).
                                                                                                                                                                                                                                                                                                                                                                                   STEROID-BINDING.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 VMCKP--GP-----ESDFCLKVEAAVIGATG------PADSQHESQHGGLDQDG- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 ----EARPALDGSAALQPLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches 66; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS0001; NUCLEAR RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Linc-finger; Steroid-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Messerle M., Rapp M., Lucin P., Koszinowski U.H.,

"Characterization of a conserved gene block in the murine
cytomegalovirus genome."

Virus Genes 10:73-80(1995).

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER BSV-1. UL54,

HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HVS-1 57, HCMV AND.MCMV
UL69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 ETSSLTESVSSSGLGEEEPPALP----SKLLSSGSCKADLGCRSYTDELHAVAP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 PACEVTSSWCLFGPELPEDPPAAPATQRVLSPLMSRSGCK--VGDSSGTAAAHKVLP 186
                                                                                                                                                                                                                                                            の数とは、ことなる数を行
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> S (IN REF. 1).
Y -> B (IN REF. 1).
S -> T (IN REF. 1).
L -> V (IN REF. 2).
80414B7F1F317F8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
rangeriptional regulator IB63 homolog (Protein UL69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine cytomegalovirus (strain Smith).
Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Beraherpesvirinae; Muromegalovirus.
NCBL_raxID-10367;
                                                                                                                                                             MODULATING, PRO-RICH. NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 95;
26.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96082764; PubMed-7483291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -JUL-1998 (Rel. 36, Created)
-JUL-1998 (Rel. 36, Last sequed)
-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L07319; AAA96666.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
   SM00399;
                                                                                                                          3D-structure
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Q69154;
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                                                                                                                                                                                             NIA BIND
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   NAME OF THE PROPERTY OF THE PR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 SRRKSSATDGRRSRRGSRRGEAQRESNGHHSSKSPST--VSSTTVHGQNGARGDSAPSRK 593
                                                                                             230 -QFIDEEPDWFERQ --- FVPFHPPPLRYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVE 285
                                                                                                                                                                                  627
                                                                                                                                                                                                                                                             342
                                                                                                                                                                                                                                                                                                                                                                                                                     343 IYDSSVPS-SELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPA-----LPSKLL 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae, Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i--CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
-i- SUBCELLUIAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS: 2 ISOFOMES; A LONG FORM (SHOM HERE) AND LEGORY FORM; ARE:PRODUCED-BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calogeraki I., Barnier J.V., Eychene A., Felder M. Pr., Calothy G.,
                                                                                                                                                           594 SQOSQQQPETTSKESSKTAAMPPPP----SP------CSPSPAS-----
                                                                                                                                                                                                                                                             286 AAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTVKAGSPSDMPRD---SG
                                                                                                                                                                                                                                                                                                                                         628 ------HDPPSGEPADAEKELATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the chicken c-rmil(B-raf-1) proto-oncogene.";
Blochem. Blophys. Res. Commun. 193:1324-1331(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- PIM: PHOSPHORYLATED.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-07-2001 (Rel. 40, Last annotation update)
RMIL serine/threonine-protein kinase (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 806 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lymphocytes, and Fibroblast;
MEDLINE-93312327; PubMed-8323553;
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476 NRMKTLGRRDSSDD 489
403 ----- LGCRSYTDE 411
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-93934;
                                                                                               •
                                                                                                                                                  P34908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 DGSAALQPLLH--TVKAGSPSDMPRDSGITDSSVPSSELSLPLMEGLSTDQTET-SSLTE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SV------SSSSGLGEEEPPALPSKLLS------SGSCKAD- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 ------GNGTDFSVSSSASTDFVASSSSSISVAPSSLSVYQNPTDMSRN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 GD-----PQLCSHLHSRDHGLQE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 NPKSPQKPIVRVFLPNKQRTVVPARCGVTVRDSLKKALADRGLIPECCAVYRIQD-GEKK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------MHQFIDEEPD------WFEKQFVPFHP-------PPLRYREP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVPPSDS--VGPPILPSPSPSRSI-----PIPQPFRPADEDHRNOFGQRDRSSSA---- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPSEIVPDFEPGPVFRGSTAGLSATPPASLPGSLTNVKALOKSPGPQRERKSSSSSEDR 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.2%; Score 93.5; DB 1; Length 806; sest Local Similarity 19.3%; Pred. No. 19; Matches 107; Conservative 55; Mismatches 165; Indels 227; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 QCPAYFLQDFCG----CEVALDLWEDFS--LCREGQREWVIQKIHESQFIIVVCSKGMKY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 FVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVY ---FDYSCE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-----GH------TRQGSRRNIFRSKSGRSLYVAICN----- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 FRCOTCGYKFHORCSTEVPLACVNYDQLDLLFVSKFFEHHPISQEETTLGETTPASGSYP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 SSESSITTAALPRERLRPRPK---VFLCISSKDG---------QNHMMVV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGSSAEGASLFNGDMEPEPPPPVLGACYAGSGGGDPAIPEEVWNIKQMIKLTQEHIEAL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 VLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 PIGWDTDISWLTGEELHVEVLENVPLTHNRVRKTFFT-----LAFCDFCRKLLFQG
                                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene; Transferase; Serine/threonine-protein kinase; Arp-binding; Nuclear protein; Alternative splicing; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISSING (IN SHORT ISOFORM).
89365 NW; 8F3FA4D5274FB75C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50081; DAG_PR_BIND_DOM_2; PROSITE; PROSILI, PROFELI KINASE APP; PROSITE; PS500101; PROFELI KINASE DOM; PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-SER
                                       InterPro; IPR002219; DAC_PE-blod.
InterPro; IPR000119; Enk_pkinase.
InterPro; IPR001116; RBD:
InterPro; IPR004040; STT_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                      D000001; Euk_pkinase; 1
                                                                                                                                                Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                                 PR00008; DAGPEDOMAIN.
                                                                                                                                                                                                                                                           SMART; SM00109; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                806 AA;
                                                                                                                                                                                                                                                                                                                        ROSITE; PS00479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
VARSPLIC
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SERIES SECTION COUNTRY PROPRIES (EC. 27.71.37).

SERIES SECTION AND PROPRIES (GALLIformes; Phasianidae; Phasianiae; Country Country of Participal Section; Control Country Country (A. 200).

SERIES SECTION AND PROPRIES (GALLIformes; Phasianiae; Country Country (A. 200).

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                                                                                                                                                                                                                                                                                                                                                                                                                        259 FRCQTCGYKFHQRCSTEVPLACVNYDQLDLLFVSKFFEHHPISQEETTLGETTPASGSYP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                             257 VLEKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPAL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 SVPPSDS--VGPPILPSPSPSKSI-----PIPQPFRPADEDHRNQFGQRDRSSSA---- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGSAALQPLLH - TVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTET - SSLTE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4 SV-----SSSSGLGEEPPALPSKLLS------SGSCKAD- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 SVPSEIVFDFEPGPVFRGSTAGLSATPPASLPGSLTNVKALQKSPGPQRERKSSSSSEDR 475
                                                                                                                                                                                                                  GD-----------VPG-----ILDLSTRYRLMDNL-PQLCSHLHSRDHGLQE 199
                                                                                                                                                                                                                                                                                                                                                   P-----GQH------TRQGSRRNYFRSKSGRSLYVAICN-----------227
                                                                                                                                                                                                                                                                                                                                                                         PIGNDIDISMLTGEELHVEVLENVPLTTHNFVRKTFFT-----LAFCDFCRKLLFQG 258
                                                                                                       1; Score 93.5; DB 1; Length 807;
1; Pred. No. 19;
55; Mismatches 165; Indels :227; Gaps
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                                                                                                                                                                                                                                                    108 FVDKKNYKHKGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVY---FDYSCE 164
                                                                                                                                                                                                                                                                            104 ------GNGTDFSVSSSASTDTVASSSSSSLSVAPSSLSVYQNPTDMSRN 147
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                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Rel. 40, Last annotation update)
SH3-containing GRB2-like protein 3 (SH3 domain protein 2C) (SH3pl3).
SH3GL3 OR SH3D2C2 OR SH3D2C.
Musrausculus (Mouse).
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MEDLINE-98294438; PubMed-9630982;

Spark A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;

"Cloning of ligand targets: systematic isolation of SH3
                                                                (IN SHORT ISOFORM).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Nurinae; Mus
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01-007-1996 (Rel. 34, Created)
01-077-1996 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Integral membrane protein DGTGZ/IDD precursor (Selzure-related
membrane-bound adhesion protein)
IDD OR DGCR2 OR DGSC OR SE212 OR SE2-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 1.2%; Score 92:5; DB 1; Length 347; Similarity! 20.7%; Pred. No. 7.8; 63; Conservative 43; Mismatches 122; Indels 77
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- STRICT CONTAINTY CONTAINTY OF THE STRAFFOLDANIN AND DYNAMIN I.

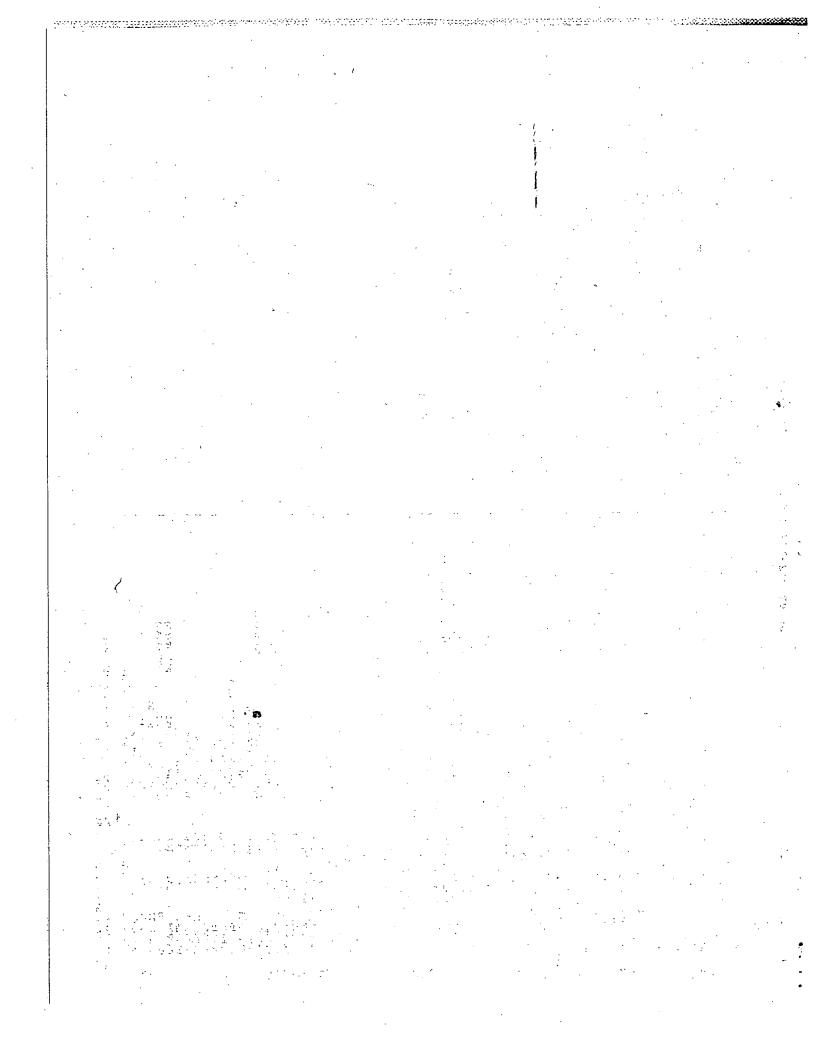
- SUBURITARITY: CONTAINS 1 SH3 DOWAIN.

- SIMILARITY: BELONGS TO THE ENDOPHILIN FAMILY.

- SIMILARITY: BELONGS TO THE ENDOPHILIN FAMILY.
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285 344 SHB:
273 276 POLY SER.
347 AA; 38934 MW; A2174642F853B5EB CRC64;
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SR3 domain; Colled Coll; Multigene family.
DOMAIN 180 201; Correst Colled Coll; Correst Colled Coll; Correst Colled Coll; Correst College Co
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ProDom; PD000066; SH3; 1.
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MGD; MGI:700011; Sh3d2c2.
InterPro; :PR001452; SH3.
Pfam; PF00018; SH3; 1;
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Search completed: May 19, 2003, 09:21:01 Job time : 14.4873 secs
    Matches
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                                                                                            Taylor C., Wadey R., O'Donnell H., Roberts C., Mattel M.-G.,
Kinber W.L., Mynshaw-Boris A., Scambler P.J.;
"Cloning and mapping of murine Dgcr2 and its homology to the Sez-12
Selzure-related protein.";
Mamm. Genome 8:371-375(1997).
                                                                                                                                                                                                                                                                                                                                    31ochem. Blophys. Res. Commun. 222:144-148(1996).
-1- FUNCTION: PROBABLY PLAYS A ROLE IN NEURAL CREST CELL MIGRATION.
MAY PLAY A ROLE IN DELIVERY OF EXTRACELLULAR SIGNALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTEGRAL MEMBRANE PROTEIN DGCR2/IDD.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
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N-LINKED (GLCNAC. .) (POTENTIAL)
P -> PE (IN REF. 2).
                                                                                                                                                                                                                   STRAIN-CS TRUE, TISSUE-Brain cortex;
KEDLINE-96212927; PubMed-8630060;
KEDLINE-96212927; PubMed-8630060;
KEDLINE-96212927; PubMed-8630060;
KLMUTA M., Sugaya E.;
Cloning of SEZ-12 encoding selzure-related and membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: UBIQUITOUS IN VARIOUS ORGANS WITH LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92.5; DB 1; Length 548;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         his SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P -> PE (IN REF. 2).
SFLG -> R (IN REF. 2).
A -> R (IN REF. 2).
77AF5CA839F6B817 CRC64;
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LDL-RECEPTOR CLASS A.
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
entities requires a license agreement (see
entities a license agreement (see
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                                                                     EDLINE-97262110; PubMed-9107688;
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Best Local Similarity
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                                    EQUENCE FROM N.A.
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ROSITE; PS50041;
NCBI_TaxID-10090;
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48; Mismatches 114; Indels 197; Gaps 24;
                                                       73 WEDFSLCREGORE-WVIQKIHESQPIIVVCSKGMKYFVDKKNYKHKGGGRGSGKG--ELF 129
                                                                                           130 L----VAVSAIAEK------ 158
                                                                                                                                                                                                              -----FDYSCEGDVPGILDLSTKYRLMDNLPQLC-SHLHSRDHGLQEPGQHTRQ---- 206
                                                                                                                                                                                                                                                                                                                                                                                                                   328 FMCLDPDGS--SLFDSMASGMRLVVSCISSFLILSLLFMVHRLAGRRRERIESLIGANL 385
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Conservative
87;
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Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Database :

Title: Perfect score:

Sednence:

Run on:

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APFLICANT: Tao, Zhengpin
APFLICANT: Spriggs, Melanie
APFLICANT: Fanslow, William
ATTLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
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OPERATING SISTEM: APPLE OWER MACINGSH
SOFTWARE: Microsoft Word for Apple, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
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Patent No. 5869286
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T: 51 University Street
Seattle
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,697-
REFERENCE/DOCKET NUMBER: 2617-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Immunex C
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1080.669 Million cell updates/sec
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Compugen Ltd.
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Length 866;

DB 2;

14.0%; Score 310;

Query Match

Sequence 50

-08-984-709A-50

Sequence

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                      .88; ... Gaps ... 20;
                                                                                                                                      70 LDLWEDFSLCREGQREWV----IQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG----- 120
                                                          14 EESSESSTYTAALPRERLRPRP----KVFLCTSSKDGONHMNVVQCFAIFLQDFCGCEVA 69
                                                                                       353 EXTSDDTKITDGLPAADLIPPPLKPRKVWIIYSA-DHPLXVDVVLKPAQFLLTACCTEVA 411
                                                                                                                                                             121 --- RGSGRGELFLVAVSALAEKLRQAKQSSSAALSKFLAVYF-DYSCEGDVPGILDLSTK 176
                                                                                                                                                                                                                                   468 RCDHGKPVGDLFTAAMMILPDFKR---;-PACFGTYVCTFSEVSCDGDVPDLFGAAPR:522
                                                                                                                                                                                                                                                                         177 KRIADNIPQICSHLHSRDHGIQEPGQHTRQG--SRRNYFRSKSGRSIXVAICNMAQFIDE 234.
                                                                                                                                                                                                                                                                                                              235 EPDWPE-----KQFVPFHPPPLKYREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEA 286
                                                                                                                                                                                                                                                                                                                                                                                       -----SQHGGLDQDGEARPALDGSA----ALQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSS 377
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CARRESPONDENCE ADDRESS:
Fred. No. 8.9e-24;
60; Mismatches 173; Indels
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FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
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51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: TAO, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, Milliam
TITLE OF INVENTION: NO. 60720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 23 MARCH 1995
/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
        28.3%;
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                             Conservative
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MEDIUM TYPE: Floppy d
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    Best Local; Similarity
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STREET: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-022-255-10
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                      Matches
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70 LDLWEDFSLCREGGREWV----IQKIHESQFIIVVCSKGMKTFVDKKNYKHKGGG----- 120
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Roslow, William
APPLICANT: No. 6072037el Receptor, That Binds IL-17
NUMBER OF SEQUENCES: 10
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MEDIUM TYPE: Floppy disk
COMPOTER: Apple Power Macintosh
OPERATING SISTEM: Apple Operating System 7.5.5
SOPTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
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; Sequence 10, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
(206)587-0430
                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                  LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: 1inear
                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-022-255-10
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CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
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177 TRLÄDNILPQICSHIHSRDHGIQEPGQHTROG--SRRNYFRSKSGRSITVAICHNHOFIDE 234 [111] [11] [11] [11] [12] 523. TPLÄDNFEEV--TFRIQDLENFOPGRÄHRVGELSGDNYLRSPGGRQIRAALDRFRDWQVR 580
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                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: Apple (PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
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FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
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Patent No. 6096305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perking, Patricia Anne-
REGISTRATION NUMBER: 134,693
REFERENCE/DOCKET NUMBER: 2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMOUNICATION INFORMATION TELEPHONE: (206) 587-0430
                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                   CITY: Seattle
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US-08-978-773-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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JS-09-022-253-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 -----PLLHTVKAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               698 GEGEACPLIGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPDLLPEDVR- 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14, EESSESSTYTAALPRERLRPRP----KVFLCYSSKDGONEMNVVQCFAYFLQDFCGCEVA 69
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                                                                                                                                                                                                                                                                                                       APPLICATION, WUMBER: USSN 08/410,535 (1) FOR THE PRICE OF THE PRICE OF
                                                                                                                                                                                                               CLASSIFICATION: 1 CONTROL OF THE CONTROL APPLICATION DATA:
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APPLICANT: Troutt, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
                                                                                                   * 日本の日本の大学の本本のでは、「なっている」
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                                                                                                                                                                                                                                                                                                                                                                                           Compara Control Control
                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION UNDERS: 34,695
REFERBICZ/COCKET UNDERS: 2617-B,
TELECOMMUNICATION: INFORMATION:
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                                                                                                                                                           APPLICATION NUMBER: 08/620,694
FILING DATE:
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ADDRESSEE: Immunex C
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                                                                     698.GEGERACPLIGSPGAG---;-RNSYLE:--LPVDPEDSPL--GSSTPMASPDLLPEDVR- 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match: 14.0%; Score 310; DB 3; Length 866; Best Local Similarity; 28.3%; Pred. No. 8.9e-24; Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps
                                          324 -----PLIMITYRAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSS 377
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638 LVGEEGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAEEGALVAAVEPGPLADGAAVRLALA
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tao, Zhengbin,
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: No.
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                                                                                                                                 378 SSGIGEEEPPALPSKLLSSGSCKADLGC 405
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APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09022260
Patent, No., 6100235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
FILLING DATE: 23, MARCH 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNET/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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CITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 RCDHGKPVGDLFTAAMMILPDFKR-----PACFGTTVVCTFSEVSCDGDVPDLFGAAPR 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 YRLMDNIPQLCSHLHSRDHGLQEPGQHTRQG--SRRNYFRSKSGRSLYVALCNMHQFIDE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 YPLADRFEEV-YFRIQDLEMFQPGRAHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVR 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 EESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVA 69
                                                                                 No. 6096305el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 866;
8.9e-24;
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60; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 310; 28.3%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: USSN 08/410,535
23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                           WSTEM: Apple Operating Sy Microsoft. Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBER: USSN 08/538,765
7 AUGUST 1995
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft, Word for ApplicURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBER: US/08/620,694
21-MARCH-1996
                                                                                                                                                         : Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Perkins, Patricia Anne
REGISTATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 261;
FELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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WEDIUM TYPE: Floppy disk
COMPUTER: Apple Fower Ma
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                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
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                                                                                                                                                            STREET: 51
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Best Local Simi
Matches 127;
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-468 RCDHGKRVGDLFTAAMMAILPDFKR----PACFGTIVVCYFSEVSCDGDVPDLFGAAPR 522
                                                                            523 YPLADRPEEV--YFRIQDLEAKTOPGRAHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVR 580
                                                                                                                                                                                                         287 AVCGATGPADSQHE------SQHGGLDQDGBARPALDGSA---ALQ 323
                                                                                                                                                                                                                                                                                                                                     698 GEGEACPLIAGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPDLLPEDVR- 745
                                                   177 FILMONLPOLCSHLHSRDHGLQEPGQHTRQG--SRRNFPRSKSGRSLTVALCNMHQFIDE 234
                                                                                                                                  235 EPDWFE-----KOFVPFHPPPLRTREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEA 286
                                                                                                                                                             638 LVGEBGGAAVAKLEPHLQPRGQPAPQPLHTLVLAAREGALYAAVEPGPLADGAAVRLALA 697
                                                                                                                                                                                                                                                                               © 324 ------PILHTYWAGSPSDMPRDSGIYDSSVPSSELSLPLARGGLSTDQTETSSLTESVSS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanle
APPLICANT: Spriggs, Melanle
APPLICANT: Ranslow, Milliam
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NOWBER OF SEQUENCES: 10
ORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                          378 SSGLGEEEPPALPSKLLSSGSCKADLGC 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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US-09-022-259-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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STREET: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70. LDLWEDFSLCREGOREWV -- - TOKTHESOFILVVCSKOMKYFVDKKNYKHKGG---- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (12.LDLLEEQAISEACYMINGRORDENVESNSKIIVICSROTR....-AKWQALLGRGAPVRL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ... - RGSGKGELFLYAVSALAEKLROAKOSSSAALSKFIAVYF, DYSCEGDVPGILDLSTK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 EPDWER------KOFVPFHPPPLRIREPVLEKFDSGLVLNDVMCKPGPESDFCLKVEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.3%; Pred. No. 8.9e-24;
ive 60; Mismatches 173; Indels 88; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 RODHGKRYGDLFTRAMMILEDFKRTTT - PACFGTYVVCTFSEVSCDGDVPDLFGAAPR 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177.TRLMDNLPQLCSHLHSRDHGLQEPGQHTRQG;;SRRNYFRSKSGRSLYVAICNMHQFIDE 234
                                                                                                                                                                                                                             SOUTH OF THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: You zhenghin APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie ATPLICANT: Ranslow, William ATPLICAT: PLIVERION: NO. 6197525el Receptor That Binds Lill. NUMBER OF SEQUENCES: 10
                                         ; DB 4; Length 866;
8.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM FAPILE OPERATING System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:
Sinilarity 28.38: prod
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STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09022257
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Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             70 LDLWEDFSLCREGOREWV----IQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG---- 120
                                                                                                                                                                                                                                                                                                                                                                                                     --- RGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYF-DYSCEGDVPGILDLSTR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 YPLADRFEEV--YFRIQDLEMFQPGRAHRYGELSGDNYLRSPGGRQLRAALDRFRDWQVR 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIMDNIPQICSHLHSRDHGLQEPGQHTRQG-.SRRNYFRSKSGRSLYVAICNMRQFIDE 234
                                                                                                                                                                                                                                                                      88; Gaps
                                                                                                                                                                                                                                                                                                          14 EESSESSTITAALPRERLRPRP ---- KVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17 NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                       SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EHLEGLMLSLFEQSLSCQAQGGC 768
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REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
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STREET: 51 University Street
CITY: Seattle
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Patent No. 5869286
                               TELECOMMUNICATION INFORMATION:
                                                                                     INFORMATION FOR SEQUID NO: (10) SEQUENCE CHARACTERISTICS (2) LENGTH: (986 amino acida (1))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yao, Zhengbin
Spriggs, Melanie
Fanslow, William
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MEDIUM TYPE: Floppy disi
                                                                                                                                                                          MOLECULE TYPE: protein US-09-022-257-10
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                                                                                                                                              amino acid
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US-08-620-694A-2
                                                                                                                                                            COPOLOGY:
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70 IDIMEDFSICREGOREWIOK --- IHESOFIIVVCSKGMKYFVDKKNYKHKGG---- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 DEEPDWFEKOFVPFHP----PPLR---TREPVLEKFDSGLVLNBVNCKFGPESSFCEKVE, 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 AAVLGATGPADSQHESQHGGLDQD-----GEARPALDGSAALQPLLH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 VCV----SERESRMAKIDPOLWPORELVAHTLOSMVLPAEQVPA---AHVVEPLHL 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 PDGSGAAAQLPMTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPMMSPDHLQGDAREQL 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finatch 13.1%; Score 289.5; DB 2; Length 864; Eocal Similarity 25.8%; Pred. No. 1.4e-21; hes 120; Conservative 75; Mismatches 170; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 EESSESSITIAALPRERLRPRP----KVFLCYSSKDGONHANVVQCFAYFLQDFCGCEVA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     William No. 6072033el Receptor That Binds IL-17 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         749 ESLALSVLQQSLSGOPLESWPRPEWVLEGCTPSEEEQRQSVQSDQG 794
                                                                                                      RIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING:DATE: 7,AUGUST 1995
                                                                                                                                                                     PRIOR APPLICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 33 MARCH 1995
APPLICATION: NUMBER:: US/08/620,694A
FILING. DATE: 21 MARCH 1996
CLASSIPITAMEN
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Sequence 2, Application 05/0902255

• Patent No. 6072033
                                                                                                                                                                                                                                                                                                                                           NAME: :Perkins; Patricia Anne.
                                                                                                                                                                                                                                                                                               ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 864 amino acida
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER
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749 ESLALSVLQQSLSGQPLESWPRPEVVLEGCTPSEEEQRQSVQSDQG 794

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414 IDILEEQVISEVGVMTWVSRQRQEMVESNSKIIILCSRG----TQAKWKAILGWAEPAV 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 DEEPDWFEKQFYPFHP----PPLR---TREPVLEKFDSGLVLADVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 289.5; DB 3; Length 864;
25.8%; Pred. No. 1.4e-21;
ive 75; Mismatches 170; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ----GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVFFDYSC-EGDVPGILDLS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 QLRCDHWKPAGDLFTAANNMILPDFKR-----PACFGTYVVCYFSGICSERDVPDLFNIT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 EESSESSTYTAALPRERLRPRP----KVFLCYSSKDGQNEMNVVQCFAYFLQDFCGCEVA 69
                                                                                                                                                                                                                                   APPLICANT: Tao, Ehengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
ITILE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOSTWARE: MICROSOFT Word for Apple, Version 6.0.1
CURRENT APPLICATION DARK
APPLICATION TOWNER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                        : Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                     Sequence 2, Application US/09022696
Patent No. 6072037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: USSN 08/FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-09-022-696-2
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CITY: Seattle.
STATE: WA.
COUNTRY: USA.
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                                                                                                                                          US-09-032-696-2
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13.1%; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.8%; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 LDLWEDFSLCREGOREWVIOR----IHESOFIIVVCSRGMRYFVDKKNYKHKGG----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 DEEPDWFEKOFVPFHP----PPLR---TREPVLEKFDSGLVLNDVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 TOCPDWFERENLCLADGODLPSLDEEVFEDPLLPP-GGGIVKQQPLVRELP-SDGCLVVD 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 AAVIGATGPADSQHESQHGGLDQD:-----GEARPALDGSAALQPLLH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 TVKAGSPSDNP--RDS-----GIYDSSV---PSSELSLPL------MEGLSTDQT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          689 PDGSGAAAQLPMTEDSEACPLIGVQRNSILCLPVDSDDLPLCSTPMMSPDHLQGDAREQL 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 IDILEEQVISEVGVMTWVSRQKQEMVESNSKIIILCSRG----TQAKWKAILGWAEPAV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ----GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSC-EGDVPGILDLS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 TKYRLADNLPQLCSHLASRDHGLQEPGQ--HTRQGSRRNYFRSKSGRSLYVALCNAHQFI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 BESSESSTYTAALPRERLRPRP----KVFLCTSSKDGQNHMNVVQCFATFLQDFCGCEVA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 ETSSLTESVSSSGLGEEEPP-----ALPSKLLSSGSCKADLG 404
                                                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Particia Anne
REGISTRATION UNDER: 34,695
REFERENCE, DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                  Corporation
CORRESPONDENCE ADDRESS:
ADDRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 864 amino acids
TYPE: amino acid
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US-09-022-255-2
                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                USA
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                                                                                                                  Seattle
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469 QLRCDHWKPAGDLFTAAMMILPDFKR-TT--PACFGTYVYCYFSGICSBRDVPDLFNIT 523
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APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word for Apple
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
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CLASSIFICATION:
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STREET: 51
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70 IDLMEDFSLCREGOREMVIOK ---- IHESOFILVVCSKGMKYFVDKKNYKHKGG----- 119
                                                                               Query Match
13.1%; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.8%; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 LDLLEEQVISEVGVMTWVSRQRQEMVESNSKIIILCSRG-----TQAKWKAILGWAEPAV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSC-EGDVPGILDLS 174
                                                                                                                                                                    328 TVKAGSPSDMP: RDS-----GIYDSSV---PSSELSLPL------MEGLSTDQT 366
                                                                                                                                                                                                           689 PDGSGAAAQLPWTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPNMSPDHLQGDAREQL: 748
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08978773

Sequence 2, Application US/08978773

Patent No. 6083906

GENERAL INFORMATION:
APPLICANT: Troutt, Anthony

TILE OF INVENTION: Method of Regulating Witric Oxide Production
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDION TYPE: Floppy:disk
COMPUTER: Apple PowerMacintosh
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM:, Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: USSN 60/052,525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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STREET: 51
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640 VCV-----SEEESRMAKLDPQIMPQRELVAHTIQSMVLPAEQVPA---AHVVEPLHL 688
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                                                                                                                                                                                                                                                                                                                                                             689 PDGSGAAAQLPMTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPWMSPDHLQGDAREQL 748
175 TKTRIADNIPQLCSHIHSRDHGLQEPGQ--HTRQGSRRNIFRSKSGRSLIVAICNAHQFI 232
                                233 DEEPDWFEKOFVPFHP----PPLR-;-TREPVLEKFDSGLVLADVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                   286 AAVIGATGPADSQHESQHGGLDQD----;-----GEARPALDGSAALQPLLH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Too. Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF ENDURCES: 10
CORRESPONDENCE ADDRESS:
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Perkins, Patricia Anne
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                                 Query Match 13.1%; Score 289.5; DB 3; Length 864;
Best Local Similarity 25.8%; Pred. No. 1.4e-21;
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 IDILLEBQVISEVGVMTWYSRQKQEMVESNSKIIILCSRG----TOAKWKAILGWAEPAV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524. SRYPLADREERV - YERIQDLEMFERGRAHHVRELTGDNYLOSPSGRQLKEAVLRFQEMQ 561
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                                                                                                                                                                                                                                                                                                    355 EKHGDDSKINGILPVADLTPPPLRPRKVWIVYSA-DHPLYVEVVLKFAQFLITACGTEVA 413
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                                                                                                                                                                              14 BESSESSTITAALPRERLRPRP----KVFLCYSSKDGONEHANVYDCFAVFLQDFCGCEVA 69
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Patent No. 6100235

GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Panslow, William
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749 ESIMILSVIQOSISGOPLESWPRPEVVIEGCIPSEEEOROSVOSDOG 794
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COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOPTWARE: Microsoft Word for Apple, Version 6.0.1
Application Data:
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APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/022,260
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO NUMBER OF, SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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STATE: WA
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STATE OF

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640 VCV-----SEEESRMAKLÜPQLHPQRELVAHTLQSMVLPAEGVPA---AHVVEPLHL 688
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Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Tao, Zhengbin
APPLICANT: Ranslow, William
APPLICANT: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 ETSSLIESVSSSSGLGEEEPP-----ALPSKLLSSGSCKADLG 404
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COMPUTER: Apple Power MacIntosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.1%; Score 289.5; DB 3; Best Local Similarity 25.8%; Pred. No. 1.4e-21; Matches 120; Conservative 75; Mismatches 170;
REGISTRATION NUMBER: 34,695
REGISTRATION NUMBER: 2617-B
REPEROMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
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51 University Street
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 864 amino acids TYPE: amino acid TOPOLOGY: linear
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 LDLWEDFSLCREGOREWVIOR----IHESOPIIVVCSKGMKYFVDKKNYKHKGG----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ----GRGSGKGELFLVAVSAIAEKIRQAKQSSSAALSKFIAVYFDYSC-EGDVPGILDLS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 TKYRLADNLPQLCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSGRSLYVALCNMHQFI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 DEEPDWFEKQFVPFHP----PPLR---YREPVLEKFDSGLVLNDVMCKPGPESDFCLKVE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AAVLGATGPADSQHESQHGGLDQD------GERARPALDGSAALQPLLH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 VCV-----SEEESRMAKLDPQLWPQRELVAHTLQSMVLPAEQVPA---AHVVEPLHL 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 TVKAGSPSDMP--RDS-----GIYDSSV---PSSELSLPL-__----NEGLSTDQT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 PDGSGAAAQLPNTEDSEACPLLGVQRNSILCLPVDSDDLPLCSTPMMSPDHLQGDAREQL 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 EESSESSITITAALPRERLRPRP----KVFLCTSSKDGQNEANVVQCFAFFLQDFCGCEVA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 ETSSLTESVSSSGLGEEEPP-----ALPSKLLSSGSCKADLG 404
                                                                                                                                                                                                           USSN 08/410,535
CURRENT/APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
                                                                                                                            08/620;694
                                                                                                                                                                                                                                                                                            . NAME:: Perkins, Patricia Anne
REGISTATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                23.MARCH 1995
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: ... (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ. ID NO. . . 2
                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE CHARACTERISTICS
LENGTH: 864 amino acids
TYPE: amino acid
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                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                    CLASSIFICATION:
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Search completed: May 19, 2003, 09:26:28 Job time : 15.3807 secs